

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
- (ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
- (iii) NUMBER OF SEQUENCES: 231
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: U.S.A.
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Sprunger, Suzanne A.
(B) REGISTRATION NUMBER: 41,323
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2043 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGAATGCCC	CATGCGCACC	CCACAGCTCG	CGCTCCTGCA	AGTGTTCCTT	CTGGTGTTC	60
CCGATGGCGT	CCGGCCTCAG	CCCTCTTCCT	CCCCATCAGG	GGCAGTGCCC	ACGTCTTTGG	120
AGCTGCAGCG	AGGGACGGAT	GGCGGAACCC	TCCAGTCCCC	TTCAGAGGCG	ACTGCAACTC	180
GCCCGGCCGT	GCCTGGACTC	CCTACAGTGG	TCCCTACTCT	CGTGACTCCC	TCGGCCCCTG	240
GGAATAGGAC	TGTGGACCTC	TTCCCAGTCT	TACCGATCTG	TGTCTGTGAC	TTGACTCCTG	300
GAGCCTGCGA	TATAAATTGC	TGCTGCGACA	GGGACTGCTA	TCTTCTCCAT	CCGAGGACAG	360
TTTTCTCCTT	CTGCCTTCCA	GGCAGCGTAA	GGTCTTCAAG	CTGGGTTTGT	GTAGACAACT	420
CTGTTATCTT	CAGGAGTAAT	TCCCCGTTTC	CTTCAAGAGT	TTTCATGGAT	TCTAATGGAA	480
TCAGGCAGTT	TTGTGTCCAT	GTGAACAACT	CAAACCTAAA	CTATTTCAG	AAGCTTCAAA	540
AGGTCAATGC	AACCAACTTC	CAGGCCCTGG	TTGCAGAGTT	TGGAGGCGAA	TCATTCACTT	600
CAACATTCCA	AACTCAATCA	CCACCATCTT	TTTACAGGGC	CGGGGACCCC	ATTCTTACTT	660
ACTTCCCCAA	GTGGTCTGTA	ATAAGCTTGC	TGAGACAACC	TGCAGGAGTT	GGAGCTGGGG	720
GACTCTGTGC	TGAAAGCAAT	CCTGCAGGTT	TCCTAGAGAG	TAAAAGTACA	ACTTGCACTC	780
GTTTTTTTCA	AGAACCTGGC	TAGTAGCTGT	ACCTTGGATT	CAGCCCTCAA	TGCTGCCTCT	840
TACTATAACT	TCACAGTCTT	AAAGGTTCCA	AGAAGCATGA	CTGATCCACA	GAATATGGAG	900
TTCCAGGTTC	CTGTAATACT	TACCTCACAG	GCTAATGCTC	CTCTGTTGGC	TGGAAACACT	960
TGTCAGAATG	TAGTTTCTCA	GGTCACCTAT	GAGATAGAGA	CCAATGGGAC	TTTTGGAATC	1020
CAGAAAGTTT	CTGTCAGTTT	GGGACAAACC	AACCTGACTG	TTGAGCCAGG	CGCTTCCTTA	1080
CAGCAACACT	TCATCCTTCG	CTTCAGGGCT	TTTCAACAGA	GCACAGCTGC	TTCTCTCACC	1140
AGTCCTAGAA	GTGGGAATCC	TGGCTATATA	GTTGGGAAGC	CACTCTTGGC	TCTGACTGAT	1200
GATATAAGTT	ACTCAATGAC	CCTCTTACAG	AGCCAGGGTA	ATGGAAGTTG	CTCTGTAAAA	1260
AGACATGAAG	TGCAGTTTGG	AGTGAATGCA	ATATCTGGAT	GCAAGCTCAG	GTTGAAGAAG	1320
GCAGACTGCA	GCCACTTGCA	GCAGGAGATT	TATCAGACTC	TTCATGGAAG	GCCCAGACCA	1380
GAGTATGTTG	CCATCTTTGG	TAATGCTGAC	CCAGCCCAGA	AAGGAGGGTG	GACCAGGATC	1440
CTCAACAGGC	ACTGCAGCAT	TTCAGCTATA	AACTGTACTT	CCTGCTGTCT	CATACCAGTT	1500
TCCCTGGAGA	TCCAGGTATT	GTGGGCATAT	GTAGGTCTCC	TGTCCAACCC	GCAAGCTCAT	1560

GTATCAGGAG TTCGATTCTT ATACCAGTGC CAGTCTATAC AGGATTCTCA GCAAGTTACA 1620
GAAGTATCTT TGACAACTCT TGTGAACTTT GTGGACATTA CCCAGAAGCC ACAGCCTCCA 1680
AGGGGCCAAC CCAAATGGA CTGGAAATGG CCATTGACT TCTTCCCTT CAAAGTGGCA 1740
TTCAGCAGAG GAGTATTCTC TCAAAATGC TCAGTCTCTC CCATCCTTAT CCTGTGCCTC 1800
TTAGAACTTG GAGTTCTCAA CCTAGAGACT ATGTGAAGAA AAGAAAATAA TCAGATTTCA 1860
GTTTTCCCTA TGAGAACTC TGAGGCAGCC ACTTATCTTG GCTAAATAGA ACCTCACCTG 1920
CTCATGACCA GAGAGCATTT AGGATAATAG AGGACCTAAC TGAAGGAATC CTTGTATATG 1980
AAAGGAGTTA TTTTAGAAAA GCAATAAAAA TATTTTATTC ATCATAAAAA AAAAAAAAAA 2040
AAA 2043

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Thr	Pro	Gln	Leu	Ala	Leu	Leu	Gln	Val	Phe	Phe	Leu	Val	Phe
1				5					10					15	
Pro	Asp	Gly	Val	Arg	Pro	Gln	Pro	Ser	Ser	Ser	Pro	Ser	Gly	Ala	Val
			20					25					30		
Pro	Thr	Ser	Leu	Glu	Leu	Gln	Arg	Gly	Thr	Asp	Gly	Gly	Thr	Leu	Gln
			35				40					45			
Ser	Pro	Ser	Glu	Ala	Thr	Ala	Thr	Arg	Pro	Ala	Val	Pro	Gly	Leu	Pro
			50				55				60				
Thr	Val	Val	Pro	Thr	Leu	Val	Thr	Pro	Ser	Ala	Pro	Gly	Asn	Arg	Thr
			65			70				75				80	
Val	Asp	Leu	Phe	Pro	Val	Leu	Pro	Ile	Cys	Val	Cys	Asp	Leu	Thr	Pro
			85					90					95		
Gly	Ala	Cys	Asp	Ile	Asn	Cys	Cys	Cys	Asp	Arg	Asp	Cys	Tyr	Leu	Leu
			100					105					110		
His	Pro	Arg	Thr	Val	Phe	Ser	Phe	Cys	Leu	Pro	Gly	Ser	Val	Arg	Ser
			115				120					125			
Ser	Ser	Trp	Val	Cys	Val	Asp	Asn	Ser	Val	Ile	Phe	Arg	Ser	Asn	Ser

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130	135	140
Pro Phe Pro Ser Arg Val Phe Met Asp Ser Asn Gly Ile Arg Gln Phe 145 150 155 160		
Cys Val His Val Asn Asn Ser Asn Leu Asn Tyr Phe Gln Lys Leu Gln 165 170 175		
Lys Val Asn Ala Thr Asn Phe Gln Ala Leu Val Ala Glu Phe Gly Gly 180 185 190		
Glu Ser Phe Thr Ser Thr Phe Gln Thr Gln Ser Pro Pro Ser Phe Tyr 195 200 205		
Arg Ala Gly Asp Pro Ile Leu Thr Tyr Phe Pro Lys Trp Ser Val Ile 210 215 220		
Ser Leu Leu Arg Gln Pro Ala Gly Val Gly Ala Gly Gly Leu Cys Ala 225 230 235 240		
Glu Ser Asn Pro Ala Gly Phe Leu Glu Ser Lys Ser Thr Thr Cys Thr 245 250 255		
Arg Phe Phe Gln Glu Pro Gly 260		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGCAGCTCA TCAACCCCTT TGGAGAGGAT GATGATGATT TTGAGACCAA CTGGATTGTC	60
GACAGGAATT TGCAGGTGTC CCTGTTGGCT GTGGATGAGA TGCACCAGGA CCTGCCTCGG	120
ATGGAGCCGG ACATGTACTG GAATAAGCCC GAGCCACAGC CCCCCTACAC AGCTGCTTCC	180
GCCCAGTTCC GTCGAGCCTC CTTTATGGGC TCCACCTTCA ACATCAGCCT GAACAAAGAG	240
GAGATGGAGT TCCAGCCCAA TCAGGAGGAC GAGGAGGATG CTCACGCTGG CATCATTTGGC	300
CGCTTCCTAG GCCTGCAGTC CCATGATCAC CATCCTCCCA GGGCAAATC AAGGACCAAA	360
CTACTGTGGC CCAAGAGGGA ATCCCTTCTC CACGAGGGCC TGCCCCAAAA CCACAAGGCA	420
GCCAAACAGA ACGTTAGGGG CCAGGAAGAC AACAAGGCCT GGAAGCTTAA GGCTGTGGAC	480
GCCTTCAAGT CTGCCCCACT GTATCAGAGG CCAGGCTACT ACAGTGCCCC ACAGACGCCC	540

CTCAGCCCCA CTCCCATGTT CTTCCCCCTA GAACCATCAG CGCCGTCAAA GCTTCACAGT 600
 GTCACAGGCA TAGACACCAA AGACAAAAGC TTAAAGACTG TGAGTTCTGG GGCCAAGAAA 660
 AGTTTTGAAT TGCTCTCAGA GAGCGATGGG GCCTTGATGG AGCACCCAGA AGTATCTCAA 720
 GTGAGGAGGA AAAGTGTGGA GTTTAACCTG ACGGATATGC CAGAGATCCC CGAAAATCAC 780
 CTCAAAGAAC CTTTGGAACA ATCACCAACC AACATACACA CTACACTCAA AGATCACATG 840
 GATCCTTATT GGGCCTTGGA AAACAGGGAT GAAGCACATT CCTAACCTGC TTCCTAATGG 900
 GGATGCTTCG CCAGCCAGGT CCTCACCTGT GTGTACACCA GCAGGACACT GATCCAGTCA 960
 CAGCCATACA GCTGTCCACA CTGAAGAACA TGTCTTACAA CAGCCTGAAT CAAATGGCTA 1020
 GCTTAATAGA TAAAAATCCC AGACTACTTC AGCCTTTAAT GCCTTTTATT CATAAAAACT 1080
 GTGAAAGCTA GACTGAACCA TTGGAAACAT TTAAGTCAGA CTCTGGATTC AGAGTCGGGA 1140
 ACCCTTAGTT CTATCTGAAT CCAAGACAGC CACACCTTAG TATACTGCCC AAAGTAATGA 1200
 GTTTAATAAA TACAAATACT CGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1260
 AAA 1263

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	His	Gln	Asp	Leu	Pro	Arg	Met	Glu	Pro	Asp	Met	Tyr	Trp	Asn	Lys
1				5				10						15	
Pro	Glu	Pro	Gln	Pro	Pro	Tyr	Thr	Ala	Ala	Ser	Ala	Gln	Phe	Arg	Arg
				20				25					30		
Ala	Ser	Phe	Met	Gly	Ser	Thr	Phe	Asn	Ile	Ser	Leu	Asn	Lys	Glu	Glu
			35				40					45			
Met	Glu	Phe	Gln	Pro	Asn	Gln	Glu	Asp	Glu	Glu	Asp	Ala	His	Ala	Gly
	50					55					60				
Ile	Ile	Gly	Arg	Phe	Leu	Gly	Leu	Gln	Ser	His	Asp	His	His	Pro	Pro
65					70					75				80	

Arg Ala Asn Ser Arg Thr Lys Leu Leu Trp Pro Lys Arg Glu Ser Leu
 85 90 95
 Leu His Glu Gly Leu Pro Lys Asn His Lys Ala Ala Lys Gln Asn Val
 100 105 110
 Arg Gly Gln Glu Asp Asn Lys Ala Trp Lys Leu Lys Ala Val Asp Ala
 115 120 125
 Phe Lys Ser Ala Pro Leu Tyr Gln Arg Pro Gly Tyr Tyr Ser Ala Pro
 130 135 140
 Gln Thr Pro Leu Ser Pro Thr Pro Met Phe Phe Pro Leu Glu Pro Ser
 145 150 155 160
 Ala Pro Ser Lys Leu His Ser Val Thr Gly Ile Asp Thr Lys Asp Lys
 165 170 175
 Ser Leu Lys Thr Val Ser Ser Gly Ala Lys Lys Ser Phe Glu Leu Leu
 180 185 190
 Ser Glu Ser Asp Gly Ala Leu Met Glu His Pro Glu Val Ser Gln Val
 195 200 205
 Arg Arg Lys Thr Val Glu Phe Asn Leu Thr Asp Met Pro Glu Ile Pro
 210 215 220
 Glu Asn His Leu Lys Glu Pro Leu Glu Gln Ser Pro Thr Asn Ile His
 225 230 235 240
 Thr Thr Leu Lys Asp His Met Asp Pro Tyr Trp Ala Leu Glu Asn Arg
 245 250 255
 Asp Glu Ala His Ser
 260

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 894 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTGAGGGT TTTTGTGTTT TTGTTTTTTC TAGGATTTC	TTGTGATGTT TTGGTTTTGT	60
TTTTTGCTTT TTGTTTAAGT TGTGCTGACA CCAAACACAT	CCAGTTTATA ATCAGTACAT	120
TGGAAAGCTG GTATTGATGT AGAACCAGTG CATAACTTTT	TATGGGGTTT TGTTATTGGT	180

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 784 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCCGCAG GTCTACTTGT GGCGAGCAGT CCAGCACAGC CTCACAGTGC AGAGCATGAG 60
CTTTGGAGCC TGCCCCCACC CTAGCTTTGT GACCTTAAGT GAGCTACATA GCTTCTCATG 120
TGTAAGTAC TCATCATAAT GGTTCTGACC TCAGTGGTTT GTTGTGTTCT AGGAAATGAT 180
GCCAGTGAAT GCGTAGTCCC AGCCTCAGCA CAGGGGAGCC ACCTTGAAGC TCTCAAATAT 240
CACTGTTGTG AATACAGAGA GGGAAAACCA ACTGTAACGT GCCACCCAAA TTTTTCAGA 300
TTAATACATC ATTCATCAGA CTTCATTCGT GATCTCGAAG AGTGACATCA GTCTTCCTTG 360
GAATATGAAG AGAATTTCTT TGGTTCTTCT TTTGCATTTC TATTTGATTT ATTTTATTTT 420
ATTTTATTTT ATGTTTTTTG GTACAGAAAG CTCATTACTA GTCCTGTCCA GCAACGTGCC 480
TCTCCTGGCC CTAGAGTTCT TGGAAATAGC CCAGGCCAAA GAGAAGGCCT TTCTCCCCAT 540
GGTCAGCCAC ACGTTCCACA TGCACACAGA GGAGTCTGAT GCCTCACAGG AGGGCGATGA 600
CCTACCCAAG TCCTCAGCAA ACACCAGCCA TCCAAGCAG GATGACAGCC CCAAGTCCTC 660
AGAAGAAACC ATCCAGCCCA AGGAGGGTGA CATCCCCAAG GCCCCAGAAG AAACCATCCA 720
ATCCAAGAAG GAGGACCTCC CCAAGTCCTC GGAAAAAGCC ATCCAGCCCA AAGAGAGTAA 780
CATC 784

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Arg Ile Ser Leu Val Leu Leu Leu His Phe Tyr Leu Ile Tyr
1 5 10 15

Phe Ile Leu Phe Tyr Phe Met Phe Phe Gly Thr Glu Ser Ser Leu Leu
 20 25 30
 Val Leu Ser Ser Asn Val Pro Leu Leu Ala Leu Glu Phe Leu Glu Ile
 35 40 45
 Ala Gln Ala Lys Glu Lys Ala Phe Leu Pro Met Val Ser His Thr Phe
 50 55 60
 His Met Arg Thr Glu Glu Ser Asp Ala Ser Gln Glu Gly Asp Asp Leu
 65 70 75 80
 Pro Lys Ser Ser Ala Asn Thr Ser His Pro Lys Gln Asp Asp Ser Pro
 85 90 95
 Lys Ser Ser Glu Glu Thr Ile Gln Pro Lys Glu Gly Asp Ile Pro Lys
 100 105 110
 Ala Pro Glu Glu Thr Ile Gln Ser Lys Lys Glu Asp Leu Pro Lys Ser
 115 120 125
 Ser Glu Lys Ala Ile Gln Pro Lys Glu Ser Asn Ile
 130 135 140

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
 AAAAAAAAAA AAAAA 75

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGAAGAAGTA GAAGCATCGA AAGCGTTGGA GAGGTGTTAC CGGAACGGCG GCGACAAGGG 60
 TGTTCCTCGAA CTAGAGTGGG GCATACATAA TCTTGCTGCT ATGCTTCGAA GCTGTAGTCT 120
 GAATCAACCT AAGTTTTTAAA CAGAAGGTGA ACCTCTGAGA TAGAAAATCA AGTATATTTT 180

AAAAGAAGGG ATGTGGGATC AAGGAGGACA GCCTTGGCAG CAGTGGCCCT TGAACCAGCA 240
 ACAATGGATG CAGTCATTCC AGCACCAACA GGATCCAAGC CAGATTGATT GGGCTGCATT 300
 GGCCCAAGCT TGGATTGCCC AAAGAGAAGC TTCAGGACAG CAAAGCATGG TAGAACAACC 360
 ACCAGGAATG ATGCCAAATG GACAAGATAT GTCTACAATG GAATCTGGTC CAAACAATCA 420
 TGGGAATTTT CAAGGGGATT CAAACTTCAA CAGAATGTGG CAACCAGAAT GGGGAATGCA 480
 TCAGCAACCC CCACACCCCC CTCCAGATCA GCCATGGATG CCACCAACAC CAGGCCCAAT 540
 GGACATTGTT CCTCCTTCTG AAGACAGCAA CAGTCAGGAC AGTGGGGAAT TTGCCCCTGA 600
 CAACAGGCAT ATATTTAACC AGAACAATCA CAACTTTGGT GGACCACCCG ATAATTTTGC 660
 AGTGGGGCCA GTGAACCAGT TTGACTATCA GGACCTCCAG GACCTCCAGC ACCTCCCCAG 720
 AATCGAAGAG AAAGGCCATC ATCATTGAGG GATCGTCAGC GTTCACCTAT TGCATTCTCT 780
 GTGAAGCAGG AGCCTCCACA AATTGACGCA GTAAAACGCA GGACTCTTCC CGCTTGGATT 840
 CGCGAAGGTC TTGAAAAAAT GGAACGTGAA AAGCAGAAGA AATTGGAGAA AGAAAGAATG 900
 GAACAACAAC GTTCACAATT GTCCAAAAAA AAAAAAAA 939

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Trp	Asp	Gln	Gly	Gly	Gln	Pro	Trp	Gln	Gln	Trp	Pro	Leu	Asn	Gln
1				5					10					15	
Gln	Gln	Trp	Met	Gln	Ser	Phe	Gln	His	Gln	Gln	Asp	Pro	Ser	Gln	Ile
			20					25					30		
Asp	Trp	Ala	Ala	Leu	Ala	Gln	Ala	Trp	Ile	Ala	Gln	Arg	Glu	Ala	Ser
		35					40					45			
Gly	Gln	Gln	Ser	Met	Val	Glu	Gln	Pro	Pro	Gly	Met	Met	Pro	Asn	Gly
	50					55					60				
Gln	Asp	Met	Ser	Thr	Met	Glu	Ser	Gly	Pro	Asn	Asn	His	Gly	Asn	Phe
65					70					75				80	
Gln	Gly	Asp	Ser	Asn	Phe	Asn	Arg	Met	Trp	Gln	Pro	Glu	Trp	Gly	Met

TTTTCTTGTT	GGCTTAGAAT	TTTCTCCAGA	AAAGCTAAGA	AAGGTGTGGA	AGATTTCCTT	660
ACAAGGGCCG	TGTTACATGA	CACTGTTAAT	GATTGCATTT	GGCTTGCTGT	GGGGGCATCT	720
CTTGCGGATC	AAACCCACGC	AGAGCGTCTT	CATTTCCACG	TGTCTGTCCT	TGTCAAGCAC	780
ACCCCTCGTG	TCCAGGTTCC	TCATGGGCAG	TGCTCGGGGT	GACAAAGAAG	GCGACATTGA	840
CTACAGCACC	GTGCTCCTCG	GCATGCTGGT	GACGCAGGAC	GTGCAGCTCG	GGCTCTTCAT	900
GGCCGTCATG	CCGACTCTCA	TACAGGCGGG	CGCCAGTGCA	TCTTCTAGCA	TTGTCGTGGA	960
AGTTCTCCGA	ATCCTGGTTT	TGATTGGTCA	GATTCTTTTT	TCACTAGCGG	CGGTTTTTCT	1020
TTTATGTCTT	GTTATAAAGA	AGTATCTCAT	TGGACCCTAT	TATCGGAAGC	TGCACATGGA	1080
AAGCAAGGGG	AACAAAGAAA	TCCTGATCTT	GGGAATATCT	GCCTTTATCT	TCTTAATGTT	1140
AACGGTCACG	GAGCTGCTGG	ACGTCTCCAT	GGAGCTGGGC	TGTTTCCTGG	CTGGAGCGCT	1200
CGTCTCCTCT	CAGGGCCCCG	TGGTCACCGA	GGAGATCGCC	ACCTCCATCG	AACCCATCCG	1260
CGACTTCCTG	GCCATCGTTT	TCTTCGCCTC	CATAGGGCTC	CACGTGTTCC	CCACGTTTGT	1320
GGCGTACGAG	CTCACGGTGC	TGGTGTTCCT	CACCTTGTC	GTGGTGGTGA	TGAAGTTTCT	1380
CCTGGCGGCG	CTGGTCCTGT	CTCTCATTCT	GCCGAGGAGC	AGCCAGTACA	TCAAGTGGAT	1440
CGTCTCTGCG	GGGCTTGCCC	AGGTCAGCGA	GTTTTCTTTT	GTCCTGGGGA	GCCGGGCGCG	1500
AAGAGCGGGC	GTCATCTCTC	GGGAGGTGTA	CCTCCTTATA	CTGAGTGTGA	CCACGCTCAG	1560
CCTCTTGCTC	GCCCCGGTGC	TGTGGAGAGC	TGCAATCACG	AGGTGTGTGC	CCAGACCGGA	1620
GAGACGGTCC	AGCCTCTGAT	GGCTCGGAGA	TGATGGACCG	TGGAAGGGAA	GCGTCTGTGG	1680
GGAGTGAGCG	CTTAGATGGC	CAGCAGCTGC	TCCTTCTGGG	AAGCTCGCAC	CTTGGCAACA	1740
GAACAGCCCT	CTAGCAGAGC	GTCAGTGCAG	TCGTGTTATC	CCGGCTTTTA	CAGAATATTC	1800
TTGTCCTATT	TTAGAATTTT	CCGGAGTAGT	TTATTTGCAG	TCTGTTGATT	ATGTGCAGTA	1860
GACCCGGGAC	ACTGCGTTTT	ACCGATCACC	TTGAATGTGG	TGCCTGGATG	TGCCTTTTTT	1920
TTTTTTCCCT	GAAATTATTA	TTAATTTTCT	ATKGKGAGTT	CATCAGTTCA	TAGTTTTTTT	1980
AGTAAAGAAG	CAAAATTAAA	AGGCTTTTAA	AAATGTACAA	CTTCAGAATT	ATAATCTGTT	2040
AGTCAAATAT	TTGTTATTAA	ACATTTCTGT	AATATGAAGT	TGTAATCCTG	GCCGTGAGCT	2100
TGGAAGCTTA	CTTTTGATTC	TTAAAGCCTA	TGTTTTCTAA	AATGAGACAA	ATACGGATGT	2160
CTATTTGCCT	TTTATTGTAA	CTTTTAAATG	AAATAATTTT	ATGTCAATTT	CTATTAGATA	2220
TATCACTTAA	AATATTTGGT	TTTAAATCAC	AAGAATATGT	ATTCTTTAAT	AAAGATAATT	2280
TATGATCATG	GTATAATTAA	TTGAAATTTA	TTAAATCTG	TTTTTATTAA	AAAAAAAAAA	2340

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 524 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Glu Leu Leu Ala Ala Glu Lys His Gln Val Glu Ala Leu Lys Asn
1              5              10              15

Met Gln His Gln Asn Gln Ser Leu Ser Met Leu Asp Glu Ile Leu Glu
                20              25              30

Asp Val Arg Lys Ala Ala Asp Arg Leu Glu Glu Glu Ile Glu Glu His
                35              40              45

Ala Phe Asp Asp Asn Lys Ser Val Lys Gly Val Asn Phe Glu Ala Val
                50              55              60

Leu Arg Val Glu Glu Glu Glu Ala Asn Ser Lys Gln Asn Ile Thr Lys
65              70              75              80

Arg Glu Val Glu Asp Asp Leu Gly Leu Ser Met Leu Ile Asp Ser Gln
                85              90              95

Asn Asn Gln Tyr Ile Leu Thr Lys Pro Arg Asp Ser Thr Ile Pro Arg
                100             105             110

Ala Asp His His Phe Ile Lys Asp Ile Val Thr Ile Gly Met Leu Ser
                115             120             125

Leu Pro Cys Gly Trp Leu Cys Thr Ala Ile Gly Leu Pro Thr Met Phe
                130             135             140

Gly Tyr Ile Ile Cys Gly Val Leu Leu Gly Pro Ser Gly Leu Asn Ser
145             150             155             160

Ile Lys Ser Ile Val Gln Val Glu Thr Leu Gly Glu Phe Gly Val Phe
                165             170             175

Phe Thr Leu Phe Leu Val Gly Leu Glu Phe Ser Pro Glu Lys Leu Arg
                180             185             190

Lys Val Trp Lys Ile Ser Leu Gln Gly Pro Cys Tyr Met Thr Leu Leu
                195             200             205

Met Ile Ala Phe Gly Leu Leu Trp Gly His Leu Leu Arg Ile Lys Pro
                210             215             220

Thr Gln Ser Val Phe Ile Ser Thr Cys Leu Ser Leu Ser Ser Thr Pro

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225		230		235		240
Leu Val Ser Arg Phe Leu Met Gly Ser Ala Arg Gly Asp Lys Glu Gly						
	245			250		255
Asp Ile Asp Tyr Ser Thr Val Leu Leu Gly Met Leu Val Thr Gln Asp						
	260		265		270	
Val Gln Leu Gly Leu Phe Met Ala Val Met Pro Thr Leu Ile Gln Ala						
	275		280		285	
Gly Ala Ser Ala Ser Ser Ser Ile Val Val Glu Val Leu Arg Ile Leu						
	290		295		300	
Val Leu Ile Gly Gln Ile Leu Phe Ser Leu Ala Ala Val Phe Leu Leu						
305		310		315		320
Cys Leu Val Ile Lys Lys Tyr Leu Ile Gly Pro Tyr Tyr Arg Lys Leu						
	325		330		335	
His Met Glu Ser Lys Gly Asn Lys Glu Ile Leu Ile Leu Gly Ile Ser						
	340		345		350	
Ala Phe Ile Phe Leu Met Leu Thr Val Thr Glu Leu Leu Asp Val Ser						
	355		360		365	
Met Glu Leu Gly Cys Phe Leu Ala Gly Ala Leu Val Ser Ser Gln Gly						
	370		375		380	
Pro Val Val Thr Glu Glu Ile Ala Thr Ser Ile Glu Pro Ile Arg Asp						
385		390		395		400
Phe Leu Ala Ile Val Phe Phe Ala Ser Ile Gly Leu His Val Phe Pro						
	405		410		415	
Thr Phe Val Ala Tyr Glu Leu Thr Val Leu Val Phe Leu Thr Leu Ser						
	420		425		430	
Val Val Val Met Lys Phe Leu Leu Ala Ala Leu Val Leu Ser Leu Ile						
	435		440		445	
Leu Pro Arg Ser Ser Gln Tyr Ile Lys Trp Ile Val Ser Ala Gly Leu						
	450		455		460	
Ala Gln Val Ser Glu Phe Ser Phe Val Leu Gly Ser Arg Ala Arg Arg						
465		470		475		480
Ala Gly Val Ile Ser Arg Glu Val Tyr Leu Leu Ile Leu Ser Val Thr						
	485		490		495	
Thr Leu Ser Leu Leu Leu Ala Pro Val Leu Trp Arg Ala Ala Ile Thr						
	500		505		510	
Arg Cys Val Pro Arg Pro Glu Arg Arg Ser Ser Leu						
	515		520			

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCAGCCCGG GCCATGCCGC ACGGCTGCTG ACCGCACGCA GGGGCCGGCC CCGAGGACAC	60
ATGCGGCGGC CTTTGCCGCC TCGCCCCTGA CCCTCTGCCC TGTTCTCCAT GTTGCATTTC	120
TCGTCAGTTT CTCGGGCGGT GTAGCTGCCG CTGCCACCAG AGCCGGCGGG GCATCGCGCT	180
GCTCATTCAT CCGGCCGCAC TTTCTTTTCC GTTTCCACCC ATCCCTTCCC ATTTCTTCT	240
CCCTTTCCCC GCCAGCTTCG CATCCATCTC CCCCACCCCG TAACCCCTCC TGCCTCCATC	300
CACCGGGGCT ATTGCCGCAA AAGA	324

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 550 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTGAACATT TCAGAAATAC AGAAGTTGAA GCAGCAGCTT ATGCAGGTAG AGCGGGAAAA	60
GGCCATTCTT TTGGCCAACC TACAGGAGTC ACAGACACAG CTGGAACACA CCAAGGGGGC	120
ACTGACGGAG CAGCATGAGC GGGTGCACCG GCTCACAGAG CACGTCAATG CCATGAGGGG	180
CCTGCAAAGC AGCAAGGAGC TCAAGGCTGA GCTGGACGGG GAGAAGGGCC GGGACTCAGG	240
GGAGGAGGCC CATGACTATG AGGTGGACAT CAATGGTTTA GAGATCCTTG AATGCAAATA	300
CAGGGTGGCA GTAAGTGAAG TGATTGATCT GAAAGCTGAA ATTAAGGCCT TAAAGGAGAA	360
ATATAATAAA TCTGTAGAAA ACTACACTGA TGAGAAGGCC AAGTATGAGA GTAAAATCCA	420
GATGTATGAT GAGCAGGTGA CAAGCCTTGA GAAGACCACC AAGGAGAGTG GTGAGAAGAT	480
GGCCACATG GAGAAGGAGT TGCAAAAGAT GACCAGCATA GCCAACGAAA ATCACAGTAC	540
CCTTAATACG	550

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Gln Val Glu Arg Glu Lys Ala Ile Leu Leu Ala Asn Leu Gln Glu
1           5           10           15

Ser Gln Thr Gln Leu Glu His Thr Lys Gly Ala Leu Thr Glu Gln His
          20           25           30

Glu Arg Val His Arg Leu Thr Glu His Val Asn Ala Met Arg Gly Leu
          35           40           45

Gln Ser Ser Lys Glu Leu Lys Ala Glu Leu Asp Gly Glu Lys Gly Arg
50           55           60

Asp Ser Gly Glu Glu Ala His Asp Tyr Glu Val Asp Ile Asn Gly Leu
65           70           75           80

Glu Ile Leu Glu Cys Lys Tyr Arg Val Ala Val Thr Glu Val Ile Asp
          85           90           95

Leu Lys Ala Glu Ile Lys Ala Leu Lys Glu Lys Tyr Asn Lys Ser Val
          100          105          110

Glu Asn Tyr Thr Asp Glu Lys Ala Lys Tyr Glu Ser Lys Ile Gln Met
          115          120          125

Tyr Asp Glu Gln Val Thr Ser Leu Glu Lys Thr Thr Lys Glu Ser Gly
          130          135          140

Glu Lys Met Ala His Met Glu Lys Glu Leu Gln Lys Met Thr Ser Ile
145           150           155           160

Ala Asn Glu Asn His Ser Thr Leu Asn Thr
          165           170

```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCCATGAGT GAATTCATCC AAGGGCACGG GTTCAGCAAG GAAAAAAGGT TAACCGTGGT

60

TCCACCAGCA AAAAGAGATT GTCAGCAGCC TGTGCTTCCG TACCGCCACA GTGTTACAA	120
CTAGCCGGGA GGCAAGACTG CCCAACTGTC AGTCCTGACA CAGCTCTCCC TGAGGAGCAG	180
CCACATTCCA GCTCCAGTG CGCCCCTCTC CACTGTCTCT CCAAGCCTCC TCACCCCTAG	240
TCTTCATCTC CTGTGGACAA ACATCTGGGG TGGAAGTTTT GTAGCCACAC ACAGGATACT	300
GCCCAAGATC CAGCGGGTGT TTTCTTCTCG GTTGTTAGAT GTACAATTGG ATTAATGTCC	360
ATCGTTTTGG AAGACGAGAG AAAGTTGAGA AGAACACGAA GCACAGACCC TGATGTGATA	420
AAACATTTTG TGGTTTCTCT GAGTCACAGA TAAACTTCTG CCATCAAATG GCTACAGTTC	480
ATTTAAATTT AAAAAAAAAA AAAAA	505

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGATACTGTA ATAAATAGGA GACAGCTACA GTGATCCAAC TAAACCAACA GGGGATTTTC	60
ATCAGCACTT CCCTGGTGTA ATCATGGTAC AGATTATTAA AGACACGAAT GAATTTAAAA	120
CATTTTTGAC AGCTGCCGGA CACAACTCG CAGTGGTTCA ATTTTCTTCG AAACGGTGTG	180
GTCCCTGCAA AAGGATGTTT CCTGTTTTCC ATGAGCTGGC TGAAACTTGT CACATCAAAA	240
CAATACCCAC ATTTCAGATG TTCAAGAAAA GCCAGAAGGT AACCTATTC TCAAGAATCA	300
AAAGAATAAT TTGCTGTTAT AGAAGTGGAT TCATGAGCAA CCTGATTTTT GAGTTTTGTG	360
GAGCCGATGC TAAAAAATTG GAAGCCAAGA CTCAAGAATT AATGTAAGCT GATCTCCAAG	420
GCAAATACA CTTGTGACAT TTGAAAAGGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	480
A	481

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

[illegible]

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1864 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

18

GTCCATCCCT TATGTAATAG TGGTTTCCCG CCCAAAGTGA GACTTTCCTT TTAATTGGAG 780
AAGGGTATAG AGGTAGTCCA GGTGGGAACG CCAGAAGTGC TGATTGCCCA GCCATTGGGA 840
CCACCTGTTC TTGCCCCACT ACCCTCTAGT GGGAGGCCAA AGTAAAGGCT GGCTGGTGGG 900
TGTCTGTGGA TTGAGGATGT GGCAGGGACT GGTCTCCCA CCTCCCTCTG GCCAAAGATG 960
GGCTTTGCCC GCTGTGTGCC TGTCACCACC CACCAGCAGT CATGCCCTGG GCTTCCCAAA 1020
TGGAGAGGTA GCAGGCAACG TTTTAAAAA GAAAGAAAAC AGGAAACTGT ATTGTGTCGG 1080
GGGAGGCGGG AGGGAGATGA GGAAACGGTT TGGATTTTGT GTGTGGGAGG GTATTTTTTG 1140
GGGGTAGTTG TCTGTAACCT TCCTAAGTGC TTTTTTTCCT TTTCTTTTTT AAAGTAAGTT 1200
GCAGGCTTTG GCTTGAAAAA CCCAGGGGG ATGGGGGGCA GAAACCTGAG GCTGCTGCCC 1260
TTTATCTGCC TTCACGGTAC TGTCCTTTC CCCAGCTCC TCCCTGACCC CATGGGCCAG 1320
GCCTCAGACC TTCCAGCTAA CCGCTTCCCA TGAGCCACTA CTCTGATGTC AGCCTATAAC 1380
CAAAGGAGCT GGGGGGTCCA GGCCTGGTGA CCAACCTTTC TCAGCCCACT CAATCAGGGT 1440
GCTCCCCACC TGCAGGCAGG AGGCAACACC CTATCTGCTA CCATCAGCCC CTTCCAGAGC 1500
CCATCTGCCC CGCCCAGCCC TGCCCTGCCC AGCCATACCC TGCTCTGCCC CATCTGGGGG 1560
TGCCCTGCTC AGGGATGGGC TGGCAGGGCT GTACCCAGCC TCCCTGGTAA GCAGAGACTC 1620
AAGAAACCTC TGGGGTCCTG TTTTCTGGTC GTGTGATCCC AGGGGTGCAC ATGGGCCCCT 1680
TGGGTGTCTG AACAGAAGGG CATGGGAGGG AGGGCTGCAC CCCTGCAGTC TTA CTCTGCT 1740
GGTGTAGCGG GCAGMTGCCC ACTCCCACCC CACCCTGCAC CGCGGGCTCC TGAGTCGGCA 1800
GATTAAGCAT TTTATAAATT GTATTTTAAA TACATGTTTT AAACCTTGTC AAAAAAAAAA 1860
AAAA 1864

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val	Leu	Pro	Thr	Cys	Arg	Gln	Glu	Ala	Thr	Pro	Tyr	Leu	Leu	Pro	Ser
1				5					10					15	
Ala	Pro	Ser	Arg	Ala	His	Leu	Pro	Arg	Pro	Ala	Leu	Pro	Cys	Pro	Ala
			20					25					30		

Ile Pro Cys Ser Ala Pro Ser Gly Gly Ala Leu Leu Arg Asp Gly Leu
35 40 45

Ala Gly Leu Tyr Pro Ala Ser Leu Val Ser Arg Asp Ser Arg Asn Leu
50 55 60

Trp Gly Pro Val Phe Trp Ser Cys Asp Pro Arg Gly Ala His Gly Pro
65 70 75 80

Leu Gly Cys Leu Asn Arg Arg Ala Trp Glu Gly Gly Leu His Pro Cys
85 90 95

Ser Leu Thr Leu Leu Val
100

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCCCTCGTA CTGATTTCCTA TCGTTGCATT TACAACTGCT AAAAAAATGC CAGCACTCCA	60
TCGACATGAA GAAGAGAAAT TCTTCTTAAA TGCCAAAGGC CAGAAAGAAA CTTTACCCAG	120
CATATGGGAC TCACCTACCA AACAACTTTC TGTCGTTGTG CCTTCAAACA ATGAAGAAAA	180
ACGGTTGCCT GTGATGATGG ATGAAGCTCT GAGCTATGTA GAGAAGAGAC AGAAACGAGA	240
TCCTGCGTTC ACTTATGAAG TGATAGTAGT TGATGATGGC AGTAAAGATC AGACCTCAAA	300
GGTAGCTTTT AAATATTGCC AGAAATATGG AAGTGACAAA GTACGTGTGA TAACCCTGGT	360
GAAGAATCGT GGAAAAGGTG GAGCGATTAG AATGGGTATA TTCAGTTCTC GAGGAGAAAA	420
GATCCTTATG GCAGATGCTG ATGGAGCCAC AAAGTTTCCA GATGTTGAGA AATTAGAAAA	480
GGGGCTAAAT GATCTACAGC CTTGGCCTAA TCAAATGGCT ATAGCATGTG GATCTCGAGC	540
TCATTTAGAA AAAGAATCAA TTGCTCAGCG TTCTTACTTC CGTACTCTTC TCATGTATGG	600
GTTCCACTTT CTGGTGTGGT TCCTTTGTGT CAAAGGAATC AGGGACACAC AGTGTGGGTT	660
CAAATTATTT ACTCGAGAAG CAGCTTCACG GACGTTTTCA TCTCTACACG TTGAACGATG	720
GGCATTGAT GTAGAACTAC TGTACATAGC ACAGTTCTTT AAAATTCCAA TAGCAGAAAT	780
TGCTGTCAAC TGGACAGAAA TTGAAGGTTT TAAATTAGTT CCATTCTGGA GCTGGCTACA	840
AATGGGTAAA GACCTACTTT TTATACGACT TCGATATTTG ACTGGTGCCT GGAGGCTTGA	900

GCAAAC TCGG AAAATGAATT AGGTTGTTTG CAGTCTTCAG TTGTGTTCTT ATGCTTCAGT 960
 GTCACATTTT ATTTTCATTTG AAAC TAAAAT TTTAAGTAAA GCTGAAATAA ACTTCTTGTC 1020
 ATTGTCAAAA AAAAAAAAAA A 1041

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Pro	Ala	Leu	His	Arg	His	Glu	Glu	Glu	Lys	Phe	Phe	Leu	Asn	Ala	1	5	10	15
Lys	Gly	Gln	Lys	Glu	Thr	Leu	Pro	Ser	Ile	Trp	Asp	Ser	Pro	Thr	Lys	20	25	30	
Gln	Leu	Ser	Val	Val	Val	Pro	Ser	Asn	Asn	Glu	Glu	Lys	Arg	Leu	Pro	35	40	45	
Val	Met	Met	Asp	Glu	Ala	Leu	Ser	Tyr	Val	Glu	Lys	Arg	Gln	Lys	Arg	50	55	60	
Asp	Pro	Ala	Phe	Thr	Tyr	Glu	Val	Ile	Val	Val	Asp	Asp	Gly	Ser	Lys	65	70	75	80
Asp	Gln	Thr	Ser	Lys	Val	Ala	Phe	Lys	Tyr	Cys	Gln	Lys	Tyr	Gly	Ser	85	90	95	
Asp	Lys	Val	Arg	Val	Ile	Thr	Leu	Val	Lys	Asn	Arg	Gly	Lys	Gly	Gly	100	105	110	
Ala	Ile	Arg	Met	Gly	Ile	Phe	Ser	Ser	Arg	Gly	Glu	Lys	Ile	Leu	Met	115	120	125	
Ala	Asp	Ala	Asp	Gly	Ala	Thr	Lys	Phe	Pro	Asp	Val	Glu	Lys	Leu	Glu	130	135	140	
Lys	Gly	Leu	Asn	Asp	Leu	Gln	Pro	Trp	Pro	Asn	Gln	Met	Ala	Ile	Ala	145	150	155	160
Cys	Gly	Ser	Arg	Ala	His	Leu	Glu	Lys	Glu	Ser	Ile	Ala	Gln	Arg	Ser	165	170	175	
Tyr	Phe	Arg	Thr	Leu	Leu	Met	Tyr	Gly	Phe	His	Phe	Leu	Val	Trp	Phe	180	185	190	
Leu	Cys	Val	Lys	Gly	Ile	Arg	Asp	Thr	Gln	Cys	Gly	Phe	Lys	Leu	Phe	195	200	205	

Thr	Arg	Glu	Ala	Ala	Ser	Arg	Thr	Phe	Ser	Ser	Leu	His	Val	Glu	Arg
210						215					220				
Trp	Ala	Phe	Asp	Val	Glu	Leu	Leu	Tyr	Ile	Ala	Gln	Phe	Phe	Lys	Ile
225					230					235					240
Pro	Ile	Ala	Glu	Ile	Ala	Val	Asn	Trp	Thr	Glu	Ile	Glu	Gly	Ser	Lys
				245					250					255	
Leu	Val	Pro	Phe	Trp	Ser	Trp	Leu	Gln	Met	Gly	Lys	Asp	Leu	Leu	Phe
			260					265					270		
Ile	Arg	Leu	Arg	Tyr	Leu	Thr	Gly	Ala	Trp	Arg	Leu	Glu	Gln	Thr	Arg
	275					280						285			
Lys	Met	Asn													
	290														

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CNCCATCGGG GAACACCAGA AAGAACACT

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TNTCTGGCAT ATCCGTCAGG TTAAACTCC

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CNCTGGTTCT ACATCAATAC CAGCTTTCC

29

- (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNACAACAGT GATATTTGAG AGCTTCAAG

29

- (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CNGTAACACC TCTCCAACGC TTTCGATGC

29

- (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCAAGGACA GACACGTGGA AATGAAGAC

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ANGTCCACCT CATAGTCATG GGCCTCCTC

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TNTCAGCCAG CTCATGGAAA ACAGGAAAC

29

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CNTGGGAAGC GGTTAGCTGG AAGGTCTGA

29

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TNTCTTCTTC ATGTCGATGG AGTGCTGGC

29

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg Val Lys Val Gln Leu Ala Leu Val Phe Phe Lys Asn Leu Ala Ser
1 5 10 15

Ser Cys Thr Leu Asp Ser Ala Leu Asn Ala Ala Ser Tyr Tyr Asn Phe
20 25 30

Thr Val Leu Lys Val Pro Arg Ser Met Thr Asp Pro Gln Asn Met Glu
35 40 45

Phe Gln Val Pro Val Ile Leu Thr Ser Gln Ala Asn Ala Pro Leu Leu
50 55 60

Ala Gly Asn Thr Cys Gln Asn Val Val Ser Gln Val Thr Tyr Glu Ile
65 70 75 80

Glu Thr Asn Gly Thr Phe Gly Ile Gln Lys Val Ser Val Ser Leu Gly
85 90 95

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTTGTACCAT	TCTTGCCAAC	TTCTGGGCTG	GCAGTATGGA	GTCATCTCCC	TATCTTTCAT	60
TGCCTGTGTG	AAATCTACTT	TCTGAATTCT	GCCATTTCCC	TCTTCACACT	GTCTCCTGGG	120
TTATCTTTGC	TTCTTCACAT	CCCTATCTCT	CTTCCTATAA	ACTGGCTCCC	GTCACTTCCA	180
TGATCCCTTC	AGTGGCTTCT	GAGCTGGTCT	CCCTGACCCC	AAAGCCTCAG	CCTTCCAGTC	240
TCCCTACAAA	ATCTCAGCAA	GTTCATTTTA	GGTTAAAATT	TGGACATATT	TTAAATACGG	300
CTCACCACCT	CATGTGAAAA	TGATGGCACC	CTACCAAGCA	GTTTGCAGAG	TTACGGTAAC	360
TGTTTCATGC	TAATGATGTT	ATTCATCCAG	TTACAATTTT	CTCAAAACTC	CTTTGGGCAC	420
TCTTTATTTT	TAATCAAATT	TTAAAGCCAA	TATTTTCATTT	TGAGAATATG	AATTAAATTG	480
GGAAATTCAT	CCTTGTGGTA	CAGTTTACAG	ATTTTTAATG	TTTACCCATT	TATCCTGTTT	540
TTTGATATAT	TAATTTCCCA	TATAGCTCCA	GAGTTATGTG	ATATTATTTT	TTTGCCAGTA	600
TATTAGAAAA	TGATTAATTT	CTCATGACCA	ACTTCTGAAA	AGAAAAGACC	AATGCAAAAT	660
GCAATCTATT	ACAATTATTT	TTTTGAATAA	AAAAGAATAT	ATTATAGTTC	TTTAACATTT	720
GATATTTTAA	ATTTGACATA	TTCTTGATAT	TTGTAAGAAA	TTTCCACTGA	ATGAATTTTA	780
CACAATTCAG	ATACTACCAA	TTAACTAATT	CTAGCCTAAA	CAAATAACAT	TATTTTTTAA	840
TAACAAAATC	TTTAAAAATA	ATTTTCTATT	TTGAACTTTT	AGCCATAATG	TAAGAAAATA	900
AAATTTTCTA	GCAGAATAAT	CAAAGAGTGA	AACAAAGTTC	CAACATGTTT	TTTCTTTGCA	960
ATTAAACATG	GCACTTTTAC	AGTTATTTAT	TATTCATATC	AGTGCACTTA	CCGACTTCAT	1020
ATTTTCAAAT	CAAAATACAG	TGTTTTTCTC	CAGTGAAATC	CTTATTCTCA	TGACTGATAG	1080
AAAACATTGC	CAATTTTGAT	ATTTCCAGAG	TTAATGTAA	ATTATTTGAA	AGAAAATTAT	1140
TTAAATAAT	AAAAATAGAC	ATTTCAAGAC	TATTTCTTAT	CACATAATTC	AAAAAGTACT	1200
TGGATCAAAT	CCTACAGAGT	TTCTCCACTA	AAATTCTACT	TGTGCAGAGG	GCATTGAAAC	1260
GCATGAAAAT	CAACAGCAGC	TTAGTTAGGT	TAATTAATTC	GGTTAATTAA	GCACCTACTA	1320
CATGCTCAGC	TCTATGCTAG	GTGTCATGAG	GAATTAAAAG	GACATGTAAT	GCACATTTTC	1380
TGATTTCAAG	GAGCTTTAAA	TATTATTGTG	TAGAAAAGT	TAACATCTAT	GAAAATAGAA	1440
GTGGGGCAAT	TTTGTGCTTA	ATTCCATGGT	CCAGATACAT	CAAAAAATCA	ATGTGGGCTG	1500

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TCAAAGAAGG TTTCTTGATA GTCATGAGTC AGCCTGATTC TTGAAAGGAT ATGTGGAATA 1560
TAAAATTTTA TTTATATTCC TTTTGAGAAA ATACTGAGAA AACCATCTTC CCTGGAAAAG 1620
AGAACGTATT GTAAAGAAAAG TACATGAAAT TGAAGGTTGA ATATCCAACA TCCCCCACAC 1680
TGCCCCAGTG TCTCTGCTCC CTTACTGAGC CTTACTATTA TTCTTCATAG CCCTATCACT 1740
ACCTAGTCTA GTATTCACTG AACTGTGTCA TCCACTAGAA TATGAGCATA ATGAGAGCAG 1800
AGACTACACC TGTCGGTTCA GTATTCTATC CTCAGCACAT AGAATGGTAC CTGGCACATA 1860
GCAGATGCTA AAATAAAATT TAAATGAATA AATTAATTCA ATCAACAAC TCAAGGTGTT 1920
ATTATTACCT ACAACTATTG TTTACAAGAG GTATGCACCG TGGAAGATCC TGGAGACACA 1980
ACAATGAATA AAGCCAAGCC AGTTCCTGCC CCCGTGGAGC TTGTAGTCAA GACATTGAAC 2040
AAGTGATCAG AAAGATGTTG ACTGCTGCAG CAGAGGGTTG CAAGCTGCTC ATGAGTATAT 2100
AACAAGTAGC CCTAACCAAA GCATTCTCTC CCTTGGTTTA ATGTCCACCC ATTGAGGTGA 2160
CTGCTAAATA CTAATCCATG ACTCTATCCC TTGGCATTCA AACTCACACA TCCACTTACC 2220
TGCCTCTCCA ACCTCATCTC CCTCCACTCA CAAGAGCCCA TCATATTATT CATCAAAATG 2280
AAACTGCACC CAGTTCTTCT GAACATATTA CTTACAAAA CTTTCATTTA TGCCTGGTGA 2340
CTCTCATCAG GCATTCAAAA GCTTTCCTC AGTGCTTCAG GGCTCTTCCT TTTCTTCCT 2400
TTATACATAC ACCTTTATGT ATCTTCATAC GTACCCTGCA TAACCTCATA TATCTTAGCA 2460
TTTACCATAT TCTGTTGAAA AACTGTTTCC ATTTCTCTTT ACTTACTAGA ATGTAAACAG 2520
ATGCACAATG TTGAGAAAAT GAAAAGTGAC AACTTTGTTT ACAAGTTTAG AAATTATCAG 2580
ATTCTCACYT AAGCTCTAGT CTCTGTAAAG TCCACAATA CTYAATAAAA GTGAAGAAAA 2640
ATGTTAACAG AGAGGGAGGA ATCAAAAACA AAGAACTATT TAAAAA AAAA 2696

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Thr Leu Ser Leu Gly Ile Gln Thr His Thr Ser Thr Tyr Leu Pro
1           5           10           15

Leu Gln Pro His Leu Pro Pro Leu Thr Arg Ala His His Ile Ile His
20           25           30

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Gln	Asn	Glu	Thr	Ala	Pro	Ser	Ser	Ser	Glu	His	Ile	Thr	Leu	Gln	Asn
	35					40					45				
Phe	His	Leu	Cys	Leu	Val	Thr	Leu	Ile	Arg	His	Ser	Lys	Ala	Phe	Pro
	50					55					60				
Gln	Cys	Phe	Arg	Ala	Leu	Pro	Phe	Leu	Pro	Phe	Ile	His	Thr	Pro	Leu
65					70					75					80
Cys	Ile	Phe	Ile	Arg	Thr	Leu	His	Asn	Leu	Ile	Tyr	Leu	Ser	Ile	Tyr
				85				90						95	
His	Ile	Leu	Leu	Lys	Asn	Cys	Phe	His	Phe	Ser	Leu	Leu	Thr	Arg	Met
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGCGCTAACT GTGCTCCTCC GGGGCCCTCC GCCTGCTCCC AGCCATGGTG GCCTGGCGCT	60
CGGCGTTCCT TGTCTGCCTC GCTTTCTCCT TGGCCACCCT GGTCCAGCGA GGATCTGGGG	120
ACTTTGATGA TTTTAACCTG GAGGATGCAG TGAAAGAAAC TTCCTCAGTA AAGCGATCAC	180
TGTAAGGATG ACATGGGAGG AGCCATGTGA AGCACTCAGC ACAGTCCTTG GAACAAGAGC	240
CATGGGACCA CACCACCACC ACCACAACCA ATAGGCCAGG AACCACCAGA GCTCCGGCAA	300
AACCTCCAGG TAGTGGATTG GACTTGGCTG ATGCTTTGGA TGATCAAGAT GATGGCCGCA	360
GGAAACCGGG TATAGGAGGA AGAGAGAGAT GGAACCATGT AACCACCACG ACCAAGAGGC	420
CAGTAACCAC CAGAGCTCCA GCAAATACTT TAGGAAATGA TTTTGACTTG GCTGATGCCC	480
TGGATGATCG AAATGATCGA GATGATGGCC GCAGGAAACC AATTGCTGGA GGAGGAGGTT	540
TTTCAGACAA GGATCTTGAA GACATAGTAG GGGGTGGAGA ATACAAACCT GACAAGGGTA	600
AAGGTGATGG CCGGTACGGC AGCAATGACG ACCCTGGATC TGGCATGGTG GCAGAGCCTG	660
GCACCATTGC CGGGGTGGCC AGCGCCCTGG CCATGGCCCT CATCGGTGCC GTCTCCAGCT	720
ACATCTCCTA CCAGCAGAAG AAGTTCTGCT TCAGCATTCA GCAGGGTCTC AACGCAGACT	780
ACGTGAAGGG AGAGAACCTG GAAGCCGTGG TATGTGAGGA ACCCCAAGTG AAATACTCCA	840
CGTTGCACAC GCAGTCTGCA GAGCCGCCGC CGCCGCCCGA ACCAGCCCCG ATCTGAGGGC	900

CCTGTCCAGC	TGCAGGCATG	CACAATGGTG	CCACCGCTTG	TCACCCGGCT	CCCCCACCC	960
CTTCATTTGG	ACCCGAGCT	GCTGTGCTGC	TCTGTGCCGT	CGGCTCCTTG	TTGGTCTGAG	1020
TTTCCCGGAT	GAGCTCTGGG	TGTTTGTGAG	TTTGGTTTCT	CTGCCCTGCC	CCAAGCGTGC	1080
TGAGACTTGG	TGCCGAAATT	CAAGAGCCAG	CTCTGATAGA	AAGCCAGCAC	CAGCCTCGGG	1140
AGCTGCTGAG	CCACCAACTC	CCAAAGCCAG	CCTGCCTCCA	GCTTTACTGA	GCACAGGATG	1200
CGGGGGCCAA	GATGATGCTG	AGGCCTGATG	ACATTTATGC	TTAGGGGACA	AGAGTTTGAA	1260
CTCAAGGGAC	TGTGACCCCT	GCACACTGGA	GTGGCTCATT	GTGGCAGGTT	TCTGCCAATA	1320
GACAGCCCCT	GACAGTGGCC	TCAAGGAGCT	GCAGGTGGGG	GGCTCAGCCT	GCACCCACTT	1380
GGAGCCCCTG	CAAGGAGCGA	ACCGGTCAGC	ACCAAGTAAC	ACCACACACA	CGCAGCACCC	1440
AGGATGATGG	TTTCACTTCA	GTCTTCCCCA	TCCCAGGTTT	TATGTTGCTG	GGCTTCCGGA	1500
GAGCCGGTCC	AAGCGGAGGC	TTTCAGTGAT	TTAAGTACAA	ACATGCATCT	CGTGATAGTC	1560
CTGCCTTGAG	AGCTTAGGAA	TCTTCCGGAT	AAGTATGAAG	CAATTCGTAG	GCCTGTTTCC	1620
CATCTGATTC	CATAGGGGGC	TGGGTGTGGC	TTCGGGTTGA	CATGAGAAAG	GTCTTTAGCA	1680
ATCATTTCTG	CACCGGAGAT	GAGTTTTATC	CTGTGTTGGG	GAGAGGTGCT	CACCCTCCAC	1740
CCTGTGTCCC	TGTTTTGGTA	GCAAGAGTGA	CCGATGTCAA	GAACGAGCAT	CAAAGCCAGA	1800
ATCCTGCTTG	TTTGCTTAAA	AATGTAATTG	GGGGCGGCGG	GGGAGGAGAG	GGGAAAGAGA	1860
CATTCGCTTG	GTTTAGTGAA	ACGCAGGTGA	CTTTGTAGCT	CTGTGGTCAG	CCTACTTGTC	1920
TGCTCTGAGG	GAGAGTGCGT	GGGAGCCAT	GCTCACCGTG	GCAAACACAG	GAACCCCATG	1980
ACTCGCCCCT	CACCTGGCGT	GGAGCTGCCT	GGTTTGGGCT	GGAGCAGAGC	TGGTTTCCTG	2040
GAATGTTTCCT	TTGGCCCACA	TATGGTTCTG	TCCCGGTGAG	CTCTGTTGTC	AGAGGCTCAC	2100
GGGACAGAAC	CACATGCTAG	GGTCTAGGGC	CCCTGTCTAC	TGATAGTCAG	TTTGCTGTGT	2160
CAGAAAGCAC	TTCTGAAAGC	AGATATGAGT	CACCAGACAG	GCAGGATCTT	ACAAAACCTCA	2220
CGGGCCTCTT	TGGTCTGCAT	GATGGCCCCA	TGCGTTTCAT	AGGCTGTCCA	CTGAGCGGGA	2280
TTGTCTGCTG	AGTGGGATGA	GCCAACTCCA	GTTTCTTAAG	GAAACCACTG	GAATCTGCAG	2340
CCCCCACATG	CATCTGTCTA	ACGCATGCCT	CGTGTTTCGTT	TTGCAAACAT	GCCTGTGGTG	2400
GAGGGTGGTC	AGTTGTAGCC	CTGTGCGTCT	CAAGGCTGCC	TTGTGAGGCC	ATTCCCAGTG	2460
CGTGCCCTTG	AGCTCCTTAC	CACCCCTTTT	CCTGCTCGGC	CCTTTAATCC	CTGACAGACC	2520
TGGACTGTGT	GGCTGAAGGG	GGACCTGCAG	CACTGCAGAA	ATGCCTCTGC	GTGGTGCCAT	2580

Asp	Gly	Arg	Arg	Lys	Pro	Gly	Ile	Gly	Gly	Arg	Glu	Arg	Trp	Asn	His	
50						55					60					
Val	Thr	Thr	Thr	Thr	Lys	Arg	Pro	Val	Thr	Thr	Arg	Ala	Pro	Ala	Asn	
65					70					75					80	
Thr	Leu	Gly	Asn	Asp	Phe	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Arg	Asn	
			85						90					95		
Asp	Arg	Asp	Asp	Gly	Arg	Arg	Lys	Pro	Ile	Ala	Gly	Gly	Gly	Gly	Phe	
			100					105					110			
Ser	Asp	Lys	Asp	Leu	Glu	Asp	Ile	Val	Gly	Gly	Gly	Glu	Tyr	Lys	Pro	
		115					120					125				
Asp	Lys	Gly	Lys	Gly	Asp	Gly	Arg	Tyr	Gly	Ser	Asn	Asp	Asp	Pro	Gly	
	130					135					140					
Ser	Gly	Met	Val	Ala	Glu	Pro	Gly	Thr	Ile	Ala	Gly	Val	Ala	Ser	Ala	
145					150					155					160	
Leu	Ala	Met	Ala	Leu	Ile	Gly	Ala	Val	Ser	Ser	Tyr	Ile	Ser	Tyr	Gln	
				165					170					175		
Gln	Lys	Lys	Phe	Cys	Phe	Ser	Ile	Gln	Gln	Gly	Leu	Asn	Ala	Asp	Tyr	
			180					185					190			
Val	Lys	Gly	Glu	Asn	Leu	Glu	Ala	Val	Val	Cys	Glu	Glu	Pro	Gln	Val	
		195					200					205				
Lys	Tyr	Ser	Thr	Leu	His	Thr	Gln	Ser	Ala	Glu	Pro	Pro	Pro	Pro	Pro	
	210					215					220					
Glu	Pro	Ala	Arg	Ile												
225																

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AATCGGGAGT	CCCAACAGCG	TTAGGTTTTT	TTTTTTGTTT	GTTTGTTTGT	TTTGTTTTTT	60
TCCAACCCTC	TTTCGGATGG	ACGGGGGAAA	GAGAGAAAGA	AAAACGAGGG	AAAATCAACA	120
AAATGTGCGA	TGCAAAGAGT	CGATTTTCGC	GGGGTTTGTC	AACTTCGCCA	CTGCCGCACG	180
CGAATCGACG	TCGTCACGTG	ACGGTCTGCC	TCCGCCCTTA	TTAACTCTCA	GCCCAGCGGC	240
GGTTTCCAGG	ACCTCAGACT	TTTTGCCGAG	GCGGCAGTCC	CTAGACGAAG	CGAAGGAGGC	300

GGCGCCTGCC CCGCCCACAA GAGCTGCCGC GCGCGGGTGT TATAGCTCCA CCCCATCTGC 360
AAAGGAAGGG GGAGCGGAAA GAGCGGGATC TAGCGTGGGA TAAAAGTGGG ACTACTACAG 420
TGTAAGTGGG CATGCGCCCC TCCTAGAAAT GATGGGAATG CAAAAGCCCT TGACTGCTCC 480
AGGACTCGAG GGATCCTCGG TGCCAGGATG CTGGGTCAAG CGCTCCGCCG GGACAGAGGA 540
CTCATACCAG GGAAATGGAG CCCAGCCTCG TGATAAACTA CGACCCAAGC TGGGGGAGGA 600
ACCTAGTTTT CGAAAGGAAA ATAATATGCG CAAGCTTTAA CTGAGCAGTG GGATGGTCTT 660
AAATACCAA GGAATGACTT TAAATCTTGC TGGATGGGAC TGCCACTCAC CGCTAGAAAT 720
CGGGGATCAA CAGCAAATC TGGATGACCC TGTAACCACA TCTCCAGTTC AGCCCGGCGA 780
GGGGCATCCT CACCCACCAG CAAAGTACCA TCCACCTTAT TGATGACAGG GATCCGGGTC 840
TCCAGGTCCA CATCAAGGTG ATTAGGCTCT TCCATGCACT CCACCTCCAG CTGCAAACCC 900
AGAATCCACC CCCATGAGCA CATACTCTTC TTTGGGGGAG GGAGGGAGGG GGAGCAGGGC 960
CAATGGTAGT CATGAAATGA CTCTAGTATT TTCCATTCCC CCAGTCCCAC TGCCTTCATC 1020
AATTATTGGG AATAAAAAGA CAATCTAATC GTCAAAAAAA AAAAAAAAAA AAAAAAA 1077

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Asp	Gly	Gly	Lys	Arg	Glu	Arg	Lys	Thr	Arg	Glu	Asn	Gln	Gln	Asn
1				5					10					15	
Val	Arg	Cys	Lys	Glu	Ser	Ile	Phe	Ala	Gly	Phe	Val	Asn	Phe	Ala	Thr
			20					25				30			
Ala	Ala	Arg	Glu	Ser	Thr	Ser	Ser	Arg	Asp	Gly	Leu	Pro	Pro	Pro	Leu
			35					40				45			
Leu	Thr	Leu	Ser	Pro	Ala	Ala	Val	Ser	Arg	Thr	Ser	Asp	Phe	Leu	Pro
	50					55				60					
Arg	Arg	Gln	Ser	Leu	Asp	Glu	Ala	Lys	Glu	Ala	Ala	Pro	Ala	Pro	Pro
65				70					75					80	
Thr	Arg	Ala	Ala	Ala	Arg	Gly	Cys	Tyr	Ser	Ser	Thr	Pro	Ser	Ala	Lys
				85				90						95	
Glu	Gly	Gly	Ala	Glu	Arg	Ala	Gly	Ser	Ser	Val	Gly				

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

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TAAGAATTAA AAATGTCATC CAAACAAGAA ATAATGAGTG ACCAGCGGTT TAGACGGGTT      60
GCAAAGGACC CGAGATTTTG GGAAATGCCA GAAAAGGATC GAAAAGTCAA AATTGACAAG      120
AGATTTTCGAG CCATGTTTCA TGACAAGAAG TTCAAGTTGA ACTATGCCGT GGATAAAAGA      180
GGGCGCCCCA TTAGCCATAG CACTACAGAG GATTTGAAGC GTTTTACGA CCTTTCAGAT      240
TCTGATTCCA ATCTCTCTGG TGAAGATAGC AAAGCATTGA GTCAAAAGAA AATAAAGAAG      300
AAAAAAACCC AGACTAAAAA AGAAATCGAT TCAAAAATC TAGTTGAGAA AAAGAAAGAA      360
ACCAAGAAGG CTAATCACAA GGGTCTGAA AATAAACTG ATTTAGATAA TTCTATAGGA      420
ATTAAAAAAA TGAAACCTC ATGTAAATTT AAGATAGATT CAAACATAAG TCCGAAGAAG      480
GATAGCAAAG AATTTACACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      540
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA      588

```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Ser Ser Lys Gln Glu Ile Met Ser Asp Gln Arg Phe Arg Arg Val
1           5           10           15

Ala Lys Asp Pro Arg Phe Trp Glu Met Pro Glu Lys Asp Arg Lys Val
          20           25           30

Lys Ile Asp Lys Arg Phe Arg Ala Met Phe His Asp Lys Lys Phe Lys
          35           40           45

Leu Asn Tyr Ala Val Asp Lys Arg Gly Arg Pro Ile Ser His Ser Thr
          50           55           60

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Thr Glu Asp Leu Lys Arg Phe Tyr Asp Leu Ser Asp Ser Asp Ser Asn
 65 70 75 80
 Leu Ser Gly Glu Asp Ser Lys Ala Leu Ser Gln Lys Lys Ile Lys Lys
 85 90 95
 Lys Lys Thr Gln Thr Lys Lys Glu Ile Asp Ser Lys Asn Leu Val Glu
 100 105 110
 Lys Lys Lys Glu Thr Lys Lys Ala Asn His Lys Gly Ser Glu Asn Lys
 115 120 125
 Thr Asp Leu Asp Asn Ser Ile Gly Ile Lys Lys Met Lys Thr Ser Cys
 130 135 140
 Lys Phe Lys Ile Asp Ser Asn Ile Ser Pro Lys Lys Asp Ser Lys Glu
 145 150 155 160
 Phe Thr Gln

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATATTTTG GTTTACTTAC TCCTCTATTT CAGAAATTGA AAAAGATCCC CAAGGATCTG	60
TTACTACTGC ATTTTCCTTCT TGCTCTGTCT ACAGCCTAGG CCAACTAGTC AGGGTCTGGA	120
CATGCATCTC CTAAAGGAAG AACTGTGTAG CACCATTGAT CACAATGTAA CATTTCATG	180
CTGCATTAAG GGTGTCTCTC TCTAATCATG ATTGTACCTG TCTCTTCCTG GGTAAGGGA	240
GATTTTTTTT TTTTAATGTG TAAAGAATTG ATGCSAGCCA GGAACATGTC TGTAAGTCCA	300
GCTACTTGGG CACACGCCTG TAGTCCMSCG CCACTCGAGC ACACACCTGT AGTACCAGCT	360
ACTCTGGAGG CTGAGGCAGG AGGATCACTT GAGCCCAGGA GATTAAGACT GTAGTATACT	420
ATGATCGTGC CTGTGGCTAG CCACTGTGCT CCAGCCTGGG CAACACCATC GTAAAAATAA	480
ATAAATAAAT AAATAAATTG GGGAGGACAG CCTCACTGGT ATCAGACTTA CAGGACCAGA	540
TAGACAAGAT GGGTATAAGG GGAGCTGAAG TCTGTGTTCA TATGAGGAAG AGAAGACCAA	600
GCCCTGGGAC TTTGGCTGAA TTCCTCCGTG GGGCTGGACG GCAGTGATCT CCTGTTCCCT	660
ATGTGTAAAC AAAGATTCCA GGGCGTGGTT TTGCACTCCT GTTGTACTCT TTAGAGGTG	720

GAAAAGAGGT	GGATACTGAG	ATCTAAGAGG	AAAGGATAGT	CATTCACGTT	CTGAGATATG	780
CGCTCTCTCT	ATTGTTCTCG	WACACAAAGG	GATAGTCTCT	TTTCTGGAGC	TGATGTCCCT	840
GCTTGGAGGT	TAGCCCCAAA	ACATGGCTCT	TGTATTGTTC	TAAGAGAAAA	GGCTTTCATT	900
TTGGTTCTTC	TGATTGGTGT	TACCTACTGC	CTAATATGTG	TTCATTTTTT	GACAGAGAGG	960
CAGACTATTG	AAAAAGTCTG	TGTGAACAGA	GAGCAGTTCA	TTAAGCCCAT	TGCTTTCAGT	1020
AATGTGGCCT	TGACCCCTTC	TGCTTCCCCC	TTCTCCCATG	GAGCATGGCA	GGGCTTGGTT	1080
ATTTAGAGTC	CATACATGCA	AGCCATTGAG	AGACTTGTTT	GCTCAAATGC	AAGTTTGCTC	1140
AAAAACAGGT	CCTGAAGGCT	TGCTTAGGAT	TACAGGGATG	CTGGGTAAGA	ACACCGTTCC	1200
TCTCTCTCGC	TGGAGAAATC	CCTGTTTCTC	TGACTCCCTT	TGTGATCCTC	ACAGTAATGT	1260
ATTCTGTGCC	ACTGTAGGAC	ACAAGGCTCT	GGGCCAGTAG	AACAGGCAGA	GAGGTGACAC	1320
TGGGCAGCAA	GCTGAGAGCT	CTTTCTAAAT	GGAGTGAAGG	AATTCAGTGG	CCTAGTTTCG	1380
CCATTCTCTA	ATGAGAAACC	AAGGCCAGGC	TGAAAAGTGC	AATTAGATGT	GGTGGATTGT	1440
GGTAACGGCC	TCCAGATAAA	GGGGTTATCC	CTGTGGAAGT	GACTTTTCCC	CATTTGATCC	1500
CTTTTCAACT	CTAAATGGCC	AGGCCCAGAG	CAGAAGAAGG	GTTGGGTCTG	GAAGGAAGGC	1560
TCCAAAGGAT	GAAAGCTTCT	CCCTGATCAT	AAGGAAGTGC	ATCTTTATAG	AATTGTTGTG	1620
CATAATGTCA	GTAAATCCCT	CTCACTTGAC	AAGGGACTGG	ATTCATCTTG	CCTTGAGACG	1680
GGCCAGTAGT	TATCAGTGAG	TCAAAGCAAA	GTGAAAGTTT	CAGGAGATGG	GACCAATGGT	1740
GCAATGCTCG	CCATAACAAA	ATTCCTTAAA	AATAAAAAAG	CTAATGTTAT	AGCAACAAAA	1800
AAAGACTGAA	GCAAAACCAC	ACTGAAATGC	ATCCCACTCC	AGGAGAGGAA	TTCTTAGCGT	1860
AACACTCTAA	ATAAATGGAA	GGAATCATCA	CCTTCCTTAT	TTTACCCCTG	CCTTGTTTAC	1920
CAGGCTGCCC	AGTGCTTACC	ATGCAGAAAG	CAGTCAGCTG	TACTCTGGAA	GTTTCTGTTC	1980
TTCTTTCCTG	GGGCTTAGGA	TATTCTGGGA	GCTGTCTGAG	CCTTGTGCCT	AAGGCTTATC	2040
AGGTGATATA	ATCTTCCTGT	TCTGGGCTGC	TTGCTGGAGG	AATAGGAAGT	GACATTTATA	2100
AGACACAGGC	GGTGTGAGCA	TCCATGTGTG	GTCTTGGTCT	AAACCAGCTC	TTGAACAGGT	2160
TAAAGCAAAC	AGCAATAACA	AAACAAAAAC	TACTGATGCT	GAGCGTTTTG	ATCCTAGTAA	2220
TATTTCAAAT	ATTGTCCTTC	TGCATATGTT	CTATCCATAT	TTGATTCCAA	TATACATTAT	2280
TAAGCTTTCT	TGGGTACTAT	TTTGCTGGGG	CTCTTGCGTG	AAGGTGGTAC	CTGTCTCATG	2340
ATCCTTAAAA	GAGAGAGGCT	TTTTTCATCC	AAAGCTGTAG	TGTTGGGAAC	TGGGGTGGGA	2400
GAGGCACTTT	TTGGAATTCT	GAAAGAATCA	TATCTGTGTA	TATACATACT	GAGTGGGGAA	2460

GGATGGGGGT TGGCAGGGGT TGAGGGAGGT GGGAACAAAC AGTGAGTATG GGAACAGGCA 2520
 GTCACCTCGA GTGTGGGAGG TCACCTGGGT CCGTCGTCTT CCTTCTGTAT GGTGTTGGGT 2580
 TTATGTACAC ACTATAACAC TTCCTGTGTG AGTTCATGTA CCTGTCTGTG AGTGCTTTGG 2640
 TGTATTGAGC CTCAGTACAC TCCAAGGGCA TTAAAGTCAA GAACTAGAAC CTGGAAAAAA 2700
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
 AAAAAAAAAA AAA 2773

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Arg	Ser	Leu	Tyr	Cys	Ser	Arg	Thr	Gln	Arg	Asp	Ser	Leu	Phe	Ser	1	5	10	15
Gly	Ala	Asp	Val	Pro	Ala	Trp	Arg	Leu	Ala	Pro	Lys	His	Gly	Ser	Cys	20	25	30	
Ile	Val	Leu	Arg	Glu	Lys	Ala	Phe	Ile	Leu	Val	Leu	Leu	Ile	Gly	Val	35	40	45	
Thr	Tyr	Cys	Leu	Ile	Cys	Val	His	Phe	Leu	Thr	Glu	Arg	Gln	Thr	Ile	50	55	60	
Glu	Lys	Val	Cys	Val	Asn	Arg	Glu	Gln	Phe	Ile	Lys	Pro	Ile	Ala	Phe	65	70	75	80
Ser	Asn	Val	Ala	Leu	Thr	Pro	Ser	Ala	Ser	Pro	Phe	Ser	His	Gly	Ala	85	90	95	
Trp	Gln	Gly	Leu	Val	Ile											100			

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAAACATTA	TGGATCTGTG	GAGCTGCTTA	TTTCCAGTGA	TGCTGATGGA	GCCATCCAAA	60
GGGCTGGAAG	ATTCAGAGTG	GAAAATGGCT	CTTCAGATGA	GAATGCAACT	GCCCTGCCTG	120
GTACTTGCG	AAGAACAGAC	GTGCACTTAG	AGAACCCAGA	ATACCACACC	AGATGGTATT	180
TCAAATATTT	TTTAGGACAA	GTCCATCAGA	ACTACATTGG	AAACGATGCC	GAGAAGAGCC	240
CTTTCTTCTT	GTCCGTGACC	CTTTCTGACC	AAAACAATCA	ACGTGTCCCT	CAATACCGTG	300
CAATTCTTTG	GAGAAAAACA	GGTACCCAGA	AAATATGCCT	TCCCTACAGT	CCCACAAAAA	360
CTCTTTCTGT	GAAGTCCATC	TTAAGTGCCA	TGAATCTGGA	CAAATTTGAG	AAAGGCCCCA	420
GGGAAATTTT	TCATCCTGAA	ATACAAAAGG	ACTTGCTGGT	TCTTGAAGAA	CAAGAGGGCT	480
CTGTGAATTT	CAAGTTTGGG	GTTCTTTTTG	CCAAAGATGG	GCAGCTCACT	GATGATGAGA	540
TGTTCAGCAA	TGAAATTGGA	AGCGAGCCTT	TTCAAAAATT	TTTAAATCTT	CTGGGTGACA	600
CAATCACTCT	AAAGGGCTGG	ACGGGCTACC	GTGGCGGTCT	GGATACCAAA	AATGATACCA	660
CAGGGATACA	TTCAGTTTAT	ACTGTGTACC	AAGGGCATGA	GATCATGTTT	CATGTTTCCA	720
CCATGTTGCC	ATATTCCAAA	GAGAACAAAC	AGCAGGTGGA	AAGGAAACGC	CACATTGGAA	780
ACGATATCGT	CACCATTGTG	TTCCAAGAAG	GAGAGGAATC	TTCTCCTGCC	TTTAAGCCTT	840
CCATGATCCG	CTCCCACTTT	ACACATATTT	TTGCCTTAGT	GAGATACAAT	CAACAAAATG	900
ACAATTACAG	GCTGAAAATA	TTTTCAGAAG	AGAGCGTACC	ACTCTTTGGC	CCTCCCTTGC	960
CAACTCCACC	AGTGTTTACA	GACCACCAGG	AATTCAGGGA	CTTTTTGCTA	GTGAAATTAA	1020
TTAATGGTGA	AAAAGCCACT	TTGGAAACCC	CAACATTTGC	CCAGAAACGT	CGGCGTACCC	1080
TGGATATGTT	GATTAGATCT	TTACACCAGG	ATTTGATGCC	AGATTGTCAT	AAGAACATGC	1140
TTAATAGACG	ATCTTTTAGT	GATGTCTTAC	CAGAGTCACC	CAAGTCAGCG	CGGAAGAAAG	1200
AGGAGGCCCG	CCAGGCGGAG	TTTGTTAGAA	TAGGGCAGGC	ACTAAACTG	AAATCCATTG	1260
TGAGAGGGGA	TGCTCCATCA	AGCTTGGCAG	CTTCAGGGAT	CTGTAAAAAA	GAGATGACCT	1320
TCCATCAGTG	CCCGTGTTTG	ACAGAACTCT	GCCAGTGAAG	CAAATGCATG	TGCTTGAGAC	1380
CCTGGACCTT	CTGGTTCTCA	GAGCAGACAA	AGGAAAAGAT	GCTCGCCTCT	TTGTCTTCAG	1440
GCTAAGTGCT	CTGCAAAAGG	GCCTTGAGGG	GAAGCAGGCT	GGGAAGAGCA	GGTCTGACTG	1500
CAGAGAAAAC	AAGTTGGAGA	AAACAAAAGG	CTGCCACCTG	TATGCTATTA	AACTCACCA	1560
CAGCAGAGAG	CTGAGGATTG	TGGTTGCAAT	TCGGAATAAA	CTGCTTCTGA	TCACAAGAAA	1620
ACACAACAAG	CCAAGCGGGG	TCACCAGCAC	CTCATTGTTA	TCTCCCCTGT	CTGAGTCACC	1680
TGTTGAAGAA	TTCCAGTACA	TCAGGGAGAT	CTGTCTGTCT	GACTCTCCCA	TGGTGATGAC	1740

CTTAGTGGAT GGGCCAGCTG AAGAGAGTGA CAATCTCATC TGTGTGGCTT ATCGACACCA	1800
ATTTGATGTG GTGAATGAGA GCACAGGAGA AGCCTTCAGG CTGCACCACG TGGAGGCCAA	1860
CAGGGTTAAT TTTGTTGCAG CTATTGATGT GTACGAAGAT GGAGAAGCTG GTTTGCTGTT	1920
GTGTTACAAC TACAGTTGCA TCTATAAAAA GGTTTGCCCC TTTAATGGTG GCTCTTTTTT	1980
GGTTCAACCT TCTGCGTCAG ATTTCCAGTT CTGTTGGAAC CAGGCTCCCT ATGCAATTGT	2040
CTGTGCTTTC CCGTATCTCC TGGCCTTCAC CACCGACTCC ATGGAGATCC GCCTGGTGGT	2100
GAACGGGAAC CTGGTCCACA CTGCAGTCGT GCCGCAGCTG CAGCTGGTGG CCTCCAGGTC	2160
GGATATATAC TTCACAGCAA CTGCAGCTGT GAATGAGGTC TCATCTGGAG GCAGCTCCAA	2220
GGGGGCCAGT GCCCGAAATT CTCCTCAGAC ACCCCCGGGC CGAGATACTC CAGTATTTCC	2280
TTCTTCCCTG GGGGAAGGTG AAATTCAATC AAAAAATCTG TACAAGATTC CACTTAGAAA	2340
CCTCGTGGGC AGAAGCATCG AACGACCTCT GAAGTCACCC TTAGTCTCCA AGGTCATCAC	2400
CCCACCCACT CCCATCAGTG TGGGCCTTGC TGCCATTCCA GTCACGCACT CCTTGTCCCT	2460
GTCTCGCATG GAGATCAAAG AAATAGCAAG CAGGACCCGC AGGGAACCTAC TGGGCCTCTC	2520
GGATGAAGGT GGACCCAAGT CAGAAGGAGC GCCAAAGGCC AAATCAAAAC CCCGGAAGCG	2580
GTTAGAAGAA AGCCAAGGAG GCCCAAGCC AGGGGCAGTG AGGTCATCTA GCAGTGACAG	2640
GATCCCATCA GGCTCCTTGG AAAGTGCTTC TACTTCCGAA GCCAACCTTG AGGGGCACTC	2700
AGCCAGCTCT GACCAGGACC CTGTGGCAGA CAGAGAGGGC AGCCCGGTCT CCGGCAGCAG	2760
CCCCTTCCAG CTCACGGCTT TCTCCGATGA AGACATTATA GACTTGAAGT AACAGAGTTG	2820
AATCTCATTT GCCATCTTTA GTTTTCTTAT GGAGGTTTAT ACTCTTTAAA CAGTTCTGAT	2880
GTAATTTCTC AACAAAATGT GGCTTTTAGC CTGTCAAGTA TCTATTGGAC CAAACCTTCT	2940
GCACACTCGG CCAGTTCCTT CTCCAATGTC CGGTGCCATC TTCCTGACC TTTGTTTCTT	3000
TCTGTTTCAGG AACCATCAGT CCCCTTGTA TAAAGGTGGT AGATTTTATT GAGGTTTTAG	3060
ATTGAACTT TGAATAAATC AAAAATACTC ATTCTTAAAA AAAAAAAAAA AAAAAAAAAA	3119

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

[illegible]

40

Cys Lys Lys Glu Met Thr Phe His Gln Cys Pro Cys Leu Thr Glu Leu
305 310 315 320

Cys Gln

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GACTTTTATA	AAAAAGTCAA	GCAGTACAAA	AGGGTGTA	GTGAAGTTAC	TGTCCTTCCC	60
CTCCATAAAC	CCCCTGACCT	TGGGAAACTG	TTGTTAACAG	TTACTTGGGT	AACTTTTCAG	120
ATATTTTGTA	TGCATGTACA	AATGTGAGTA	TCTAATGTAA	AAAAATCAAA	CCAAGATAAA	180
GTGTAAACTG	CTATGATGGA	ATCCTGCCTT	GTTCTGCTAT	TAGTCTTCTG	TTTAATAATC	240
AGCTTTGGTA	TTAGGACAGT	GGTAGGAAGA	AGCCAGTATG	TCCTGCAACA	TAATTTGTGG	300
TTCTGGACTG	GTCAGGATTT	CCTGAATGCA	GCCTTTATCT	GGAAGCTCTG	CCCTTCTCCA	360
TCTGGGATAC	GCTTTTTTCAT	CCATCAAAAC	TGTCATCTCC	CTCTGTGAAG	CCTTCCCTGA	420
CTATTCTCTG	TCCCTCTTTC	CTCTCTTCCC	ACAAACACAA	CTGTGTACGC	GTGTCACCAA	480
AGAGTTAATC	GTGCTTTTCT	CTGTGCTACT	TTTATACSTA	GTATATGGTC	CATTGTTTTG	540
CACTTAATAC	ACTCTCTTGT	AATGATTTGT	TTACATGTCA	GTCTCCCAGC	CAGACTGAGA	600
GCTCACCAAG	GGCAGAAGCC	GTGTTTTGTT	TACTGCTGTA	TTCTGGTAC	CTGGTACAAT	660
GCTTGGCATA	CAGTTGGATG	AACGGGAAAG	TAATCTGAGC	TGCCGGTGCT	GTGGCAGTGC	720
AAAGTGGGCA	TATTTGTGCC	CTTGGACCAG	ATGTAGCCCT	TGATGCATTT	TGCAGGAACA	780
CGGCTTAGTT	ATTGTTTACT	TTGAAGCCCT	TTTGCCTCTA	CTCTCTCCCA	TATATCTTCT	840
CCTGACAGGG	TGAAGTCACC	TATAGCATTT	CCTAGTGTAT	GGAAGTATTA	ATTTCTTTCT	900
TTACTGGAAG	AGCTACTAGC	TTTTCTTCAT	ACAGTTTCCT	CTGCTCCAGT	TTCATAAGTT	960
TCTTTTTTGGC	TTGTATCTGT	TTAGGATCAG	GTGATATGGC	TTCATTTCTC	ATGACTGAAG	1020
CCCGGCAACA	TAACACTGAA	ATTCGAATGG	CAGTCAGCAA	AGTGGCTGAT	AAAATGGATC	1080
ATCTCATGAC	TAAGGTTGAA	GAGTTACAGA	AACATAGTGC	TGGCAATTCC	ATGCTTATTC	1140

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CTAGCATGTC AGTTACAATG GAAACAAGCA TGATTATGAG CAACATCCAG CGAATCATTC      1200
AGGCCAAGGT GACAGAGGAG TTAGCAGCGG CCACTGCACA GKTCTCTCAT CTGCAGCTGA      1260
AAATGACTTG CTCACCAAAA AAAGGAAACA GAGCTGCAGA TGCAGCTGAC AGAAAGCCTG      1320
AAGGAGACAG ATCTTCTCAG GGGCCAGCTC ACCAAAGTGC AGGCAAAGCT CTCAGAGCTC      1380
CAAGAAACYT CTGAGCAAGC ACAGTCCAAA TTCAAAAGTG AAAAGCAGAA CCGGAAACAA      1440
CTGGAActCA AGGTGACATC CCTGGAGGAG GAACTGACTG ACCTTCGAGT TGAGAAGGAG      1500
TCCTTGAAA AGGTAAGCTC TACAACCCAG TTTGCCAGAA TTAGCTGTTT AATAAACATT      1560
TTTATTTTCC TTTTACAAAA AAAAAAAAAA AA                                  1592

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(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Met Glu Val Leu Ile Ser Phe Phe Thr Gly Arg Ala Thr Ser Phe Ser
1           5           10           15

Ser Tyr Ser Phe Leu Cys Ser Ser Phe Ile Ser Phe Phe Leu Ala Cys
          20           25           30

Ile Cys Leu Gly Ser Gly Asp Met Ala Ser Phe Leu Met Thr Glu Ala
          35           40           45

Arg Gln His Asn Thr Glu Ile Arg Met Ala Val Ser Lys Val Ala Asp
          50           55           60

Lys Met Asp His Leu Met Thr Lys Val Glu Glu Leu Gln Lys His Ser
65           70           75           80

Ala Gly Asn Ser Met Leu Ile Pro Ser Met Ser Val Thr Met Glu Thr
          85           90           95

Ser Met Ile Met Ser Asn Ile Gln Arg Ile Ile Gln Ala Lys Val Thr
          100          105          110

Glu Glu Leu Ala Ala Ala Thr Ala Gln Xaa Ser His Leu Gln Leu Lys
          115          120          125

Met Thr Cys Ser Pro Lys Lys Gly Asn Arg Ala Ala Asp Ala Ala Asp
          130          135          140

Arg Lys Pro Glu Gly Asp Arg Ser Ser Gln Gly Pro Ala His Gln Ser
145          150          155          160

```

Ala Gly Lys Ala Leu Arg Ala Pro Arg Asn Xaa
165 170

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1694 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGAAACGGG AAGCCGCTGC AAGTCCACCG CCTCAGCTAC CCAGATTGGG ATCTGCCCAG	60
GCCCCTTTTA TGGACTAGTG TGGGCGGCAG GCTCCTTTCC GTCCCTGCCC TGCTGTACCC	120
CGCTCCTTGG AGACCCCCTG TATCCCTCCC GCAAGGTGGA ATCCGCAGGC TGGAGGCTCC	180
CAGGGGAGGC AAACGCCTGG CCCTGCCCTG CCCCACGCCG CACCATGACC CTCCTGCTGC	240
TGCCCCTTCT GCTGGCCTCT CTGCTCGCGT CCTGCTCCTG TAACAAAGCC AACAAGCACA	300
AGCCATGGAT TGAGGCAGAG TACCAGGGCA TCGTCATGGA GAATGACAAC ACGGTCTCTAC	360
TGAATCCACC ACTCTTTGCC TTGGACAAGG ATGCCCCGCT GCGCTATGCA GGTGAGATCT	420
GCGGCTTCCG GCTCCATGGG TCTGGGGTGC CTTTGAGGC TGTGATCCTT GACAAGGCGA	480
CAGGAGAGGG GCTGATCCGG GCCAAGGAGC CTGTGGACTG CGAGGCCCAG AAGGAACACA	540
CCTTCACCAT CCAGGCCTAT GACTGTGGCG AGGGCCCCGA CGGGGCCAAC ACCAAGAAGT	600
CCCACAAGGC CACTGTGCAT GTGCGGGTCA ACGATGTGAA CGAGTTTGCC CCAGTGTTTG	660
TGGAACGGCT GTATCGTGCG GCTGTGACAG AGGGGAAGCT GTACGATCGC ATCCTGCGGG	720
TGGAAGCCAT TGACGGTGAC TGCTCCCCC AGTACAGCCA GATCTGCTAC TATGAGATTC	780
TCACACCCAA CACCCCTTTC CTCATTGACA ATGACGGGAA CATTGAGAAC ACAGAGAAGC	840
TGCAGTACAG TGGTGAGAGG CTCTATAAGT TTACAGTGAC AGCTTATGAC TGTGGGAAGA	900
AGCGGGCAGC AGATGATGCT GAGGTGGAGA TTCAGGTGAA GCCCACCTGT AAACCCAGCT	960
GGCAAGGCTG GAACAAAAGG ATCGAATATG CACCAGGTGC TGGGAGCTTG GCTTTGTTCC	1020
CTGGTATCCG CCTGGAGACC TGTGATGAAC CACTCTGGAA CATTCAGGCC ACCATAGAGC	1080
TGCAGACCAG CCATGTGGCC AAGGGCTGTG ACCGTGACAA CTACTCAGAG CGGGCGCTGC	1140
GGAAACTCTG TGGTGCTGCC ACTGGGGAGG TGGATCTGTT GCCCATGCCT GGCCCCAATG	1200
CCAAGTGGAC AGCAGGACTC TCGGTGCACT ACAGCCAGGA CAGCAGCCTG ATCTACTGGT	1260

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TCAATGGCAC CCAGGCTGTG CAGGTGCCCC TGGGTGGCCC CAGTGGGCTG GGCTCTGGGC      1320
CCCAGGACAG CCTCAGTGAC CACTTCACCC TGTCTTCTG GATGAAGCAT GGCCTAAGTC      1380
CCAACAAGGG CAAGAAGGAA GAGGAAACCA TCGTATGTAA CACTGTCCAG AATGGTGAGC      1440
CTCCCCCTCCA GGCCTAGACC AGAGGGGGAA ACTGGCTTCT TGTCCCGCCT CTGTCACTGC      1500
CCAGTGTGTG ACTGTGAACA GGTCACCTCC CCTCTCTTCA TTTGTGAGGT GCAAGTGCCA      1560
GGTGTGATAT GCCTTGATTC TGTGCTTTAT CCCCAACATG ACATGTTGGA TCGTAAAAAA      1620
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      1680
AAAAAAAAAA AAAA                                             1694

```

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Met Thr Leu Leu Leu Leu Pro Leu Leu Leu Ala Ser Leu Leu Ala Ser
1           5           10           15

Cys Ser Cys Asn Lys Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu
          20           25           30

Tyr Gln Gly Ile Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro
          35           40           45

Pro Leu Phe Ala Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu
          50           55           60

Ile Cys Gly Phe Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val
65           70           75           80

Ile Leu Asp Lys Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro
          85           90           95

Val Asp Cys Glu Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr
          100          105          110

Asp Cys Gly Glu Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys
          115          120          125

Ala Thr Val His Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val
          130          135          140

Phe Val Glu Arg Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr

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145		150		155		160
Asp Arg Ile Leu Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln						
	165			170		175
Tyr Ser Gln Ile Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe						
	180			185		190
Leu Ile Asp Asn Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr						
	195			200		205
Ser Gly Glu Arg Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly						
	210			215		220
Lys Lys Arg Ala Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro						
	225			230		235
Thr Cys Lys Pro Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala						
	245			250		255
Pro Gly Ala Gly Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr						
	260			265		270
Cys Asp Glu Pro Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr						
	275			280		285
Ser His Val Ala Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala						
	290			295		300
Leu Arg Lys Leu Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro						
	305			310		315
Met Pro Gly Pro Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr						
	325			330		335
Ser Gln Asp Ser Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val						
	340			345		350
Gln Val Pro Leu Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp						
	355			360		365
Ser Leu Ser Asp His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val						
	370			375		380
Thr Pro Asn Lys Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr						
	385			390		395
Val Gln Asn Gly Glu Pro Pro Leu Gln Ala Leu Ala Arg Gly Gly Asn						
	405			410		415
Trp Leu Leu Val Pro Pro Leu Ser Leu Pro Ser Val						
	420			425		

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1309 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGGTCCTCC TTTGCAGAGG TGGTGCGGAG CTCCTGTTTG ACGGTATTAA GAAACATCGA	60
GTCACCTTGC CTGGACAGGA GGAACCCTGG GACATCCGGA ACCTGCTCAT CTGGATCAAG	120
AAGAATTTGC TAAAAGAGCG GCCAGAGTTG TTCATCCAGG GAGACAGCGT GCGGCCAGGA	180
ATTCTGGTGC TGATTAACGA TGCCGACTGG GAGCTACTGG GTGAGCTGGA CTACCAGCTT	240
CAGGACCAGG ACAGCGTCCT CTTTCATCTCC ACTCTGCACG GCGGCTGAGG GCCCTTCTCT	300
GGGCCTGGGC ACCCTTAGAG GGGAGAACGA AGCAATCAGA CATCCCCTTG GGCCCTGCTT	360
CCAGGTCTCC CTGTCCCCCT TGCCTGCCTT CTTCCCTGCT CTGTCCCCTA AGCTCCCTCC	420
AGGCAGGGAA AAGAGGCCAG GTGCTAAAAA TGAGCCTTTC TCAAGCACGT GAGCAGCGGA	480
AGGCAGACAG GCGCCAGAGC CCAGCACTCC CTTTTCCAGC AGCTGTGGTG GGGGAGGGTT	540
CCCCTCCAGT TTGTCAAGAG TTGAAGGAGG CTCTGTGGCC AGGTGACCTG GCTGCCTTCC	600
ACTCCTTGTA CCTCAGTCTA AACATGGAGT GGCCGCTGAC AAGGCGCTCC AGCCCCAGAG	660
CCAGCGTCTT CATGGGGAAG ATGAATGGAC CTGAGTAGCT GAAGGAAGGC CCCTCCCTAC	720
CCAAAGACTG GAGGCTTCTC AGCCTCAATT TCCCTGTCTG TACAGCTGAG GGCTCTGCCT	780
GTCCCCCACT GCTATCAGTA TGGAACCCCA GCTGGGGTCC CCTATTGAGT GCCGACTCCC	840
CCCACCGCCA GCAGCTGCTC CTCCAGCCAC ACCCTTCCTG CTCCCCCCAC CCYTAGCCCT	900
TGACCCTGGC TGGCCTGCCC CGCTCCACAG GCCACCAGAT GGGCTCCTGA GACCCTCCCC	960
AGGCTGCTTA CAGCTCATTC TGCTGGGGGT AGAGATGAGG GGAGGGAGTA AGTTAAACCT	1020
TGGACTAGCA AGTAGAAGCC TGGGGGGATG CGTGTGCCTC AGTTTCCTCC TCCACAACCTG	1080
AATATAGTGG CTGAAAACCTG GGGAGATACT TGATGGCGCG AATGTCCGTT TTCTCTCCCT	1140
TCCCACCTCC TGCAGGAAGC AGGACGGGGC AGGCAGCACC TGGTAGGCAC AGTGCTTTGC	1200
CCCTCCTCCC CTTCCCTTCT GGAAGTCTTG GGGCCTCAGT GCTTGCAACA GCCGGCCTTG	1260
GGCAAATAAA AGACTAGGTT GTTTACTAAA AAAAAAAAAA AAAAAAAAAA	1309

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Met Ala Arg Met Ser Val Phe Ser Pro Phe Pro Pro Pro Ala Gly Ser
1           5           10           15

Arg Thr Gly Gln Ala Ala Pro Gly Arg His Ser Ala Leu Pro Leu Leu
          20           25           30

Pro Phe Pro Ser Gly Ser Leu Gly Ala Ser Val Leu Ala Thr Ala Gly
          35           40           45

Leu Gly Gln Ile Lys Asp
          50

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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

GGCCCGTGCG CTCCATCAAC CACGCCAGCC TCATCTCTGC ACTCTCCCGG GACTATCGCA      60
ACCTGAAGCC CAGTGCTGTT GCCCCACAGA GAAAGATGCC ACTGGATGAC ACCAAACTGA      120
TTATCCACCA GAACTCAGC GTCTTAGAAG ATATTGTGGA GAATATCTCG GGGGAGTCCA      180
CCAAGTCTCG ACAGATTTGC TACCAGTCGC TGCAGGAATC TGTTTCAGGTC TCCCTGGCCC      240
TCTTTCCAGC TTTTATCCAT CAGTCAGATG TGAATGATGA GATGCTGAGC TTCTTCCTCA      300
CTCTGTTTTG AGGCCTTAGA GTACAGATGG GTGTGCCTTT CACTGAGCAA ATCATAACAGA      360
CTTTCTCTCA CATGTTTACC AGAGAGCAGT TAGCCGAGAG CATCCTCCAC GAGGGCAGCA      420
CAGGCTGCCG GGTGGTGGAG AAGTTTCTGA AGATCCTGCA GGTGGTGGTC CAGGAGCCAG      480
GCCAGGTGTT CAAGCCCTTC CTCCCCAGCA TCATCGCCCT GTGCATGGAG CAAGTGTATC      540
CCATCATTGC CGAGCGTCCC TCCCCTGATG TGAAGGCCGA GCTGTTTGAG CTCCTTTTCC      600
GGACGCTCCA TCACAACTGG AGGTACTTCT TCAAGTCCAC CGTGCTGGCC AGTGTCCAGA      660
GGGGGATCGC TGAGGAGCAG ATGGAGAATG AGCCCCAGTT CAGTGCCATC ATGCAGGCTT      720
TCGGACAGTC CTTTCTCCAG CCCGACATCC ACCTTTTAA ACAAATCTC TTCTACTTGG      780

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AGACTCTCAA CACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT GCCATGCTGT 840
TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT CTTCTGCAGG 900
AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA CTTTGATGGC TTCTTTGCCG 960
CCTTCCTCCC AGAGTTCCTG ACCAGCTGTG ATGGTGTGGA TGCCAACCAG AAAAGTGTGC 1020
TGGGGCGGAA TTTCAAGATG GATCGGGACC TGCCCTCATT CACCCAGAAT GTGCACAGGC 1080
TGGTCAACGA CCTGCGCTAC TACAGACTCT GCAACGACAG CCTGCCCCCT GGCAGTGTGA 1140
AGCTCTAGGC CTGCTACTGC CTGGGGACAC GGACTTCTGC TGCTGCCACC TGCGCCAGCC 1200
CTACCTTCCA CCACAGATGT CTCCCAGATG GGCCTTGCTC ACACTCCTTG GCTTCTCCCA 1260
CCGCAAGCAA CGCTGCCTGC CTCTGCCGCT CCTCCACATC TTGCCGCTGC CCAGCAGAGC 1320
TGGCTTCTGG GTCCACCTGA GCACTGGACG GTGCTCCCAG GGCGTTGGAG CAGGCGGAGG 1380
GGTGTGTGGC CAGGTACTAG GAGGCACCAG GAAATCCCGC GGGGTGGCCC ATGCAGACCA 1440
GGCGCACGTG GCTCATGGGG CAGAATTGCC AAGGACAGCT CACGACAGTG CMACCTTCTC 1500
ACCATTCCAG CCAAGGAGAG ATGTGACGTT GGAAMTGYTY TGGCAMTTYT GTCAAGCCTC 1560
CCCCGCCCCA ATTGCCTTGA RATYTYTGCT CTTTGTGAGA GATTTGCAAA GACTCAMGTT 1620
TTTGTTGTTT TCTCATCATT CCATTGTGAT ACTAAGAAAC TAAGAAGCTT AATGAAAAGA 1680
AATAAAATGC CTATGTTGTT GTTCTAGGRR AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1740

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Pro	Leu	Asp	Asp	Thr	Lys	Leu	Ile	Ile	His	Gln	Thr	Leu	Ser	Val
1				5				10					15		
Leu	Glu	Asp	Ile	Val	Glu	Asn	Ile	Ser	Gly	Glu	Ser	Thr	Lys	Ser	Arg
		20					25						30		
Gln	Ile	Cys	Tyr	Gln	Ser	Leu	Gln	Glu	Ser	Val	Gln	Val	Ser	Leu	Ala
		35				40						45			
Leu	Phe	Pro	Ala	Phe	Ile	His	Gln	Ser	Asp	Val	Thr	Asp	Glu	Met	Leu
	50					55					60				

Ser 65	Phe	Phe	Leu	Thr	Leu 70	Phe	Arg	Gly	Leu	Arg	Val	Gln	Met	Gly	Val 80
Pro	Phe	Thr	Glu	Gln 85	Ile	Ile	Gln	Thr	Phe	Leu	Asn	Met	Phe	Thr 95	Arg
Glu	Gln	Leu	Ala 100	Glu	Ser	Ile	Leu	His 105	Glu	Gly	Ser	Thr	Gly	Cys 110	Arg
Val	Val	Glu 115	Lys	Phe	Leu	Lys	Ile	Leu	Gln	Val	Val	Val	Gln	Glu	Pro
Gly	Gln 130	Val	Phe	Lys	Pro	Phe 135	Leu	Pro	Ser	Ile	Ile 140	Ala	Leu	Cys	Met
Glu 145	Gln	Val	Tyr	Pro	Ile 150	Ile	Ala	Glu	Arg	Pro 155	Ser	Pro	Asp	Val	Lys 160
Ala	Glu	Leu	Phe 165	Glu	Leu	Leu	Phe	Arg	Thr 170	Leu	His	His	Asn	Trp 175	Arg
Tyr	Phe	Phe	Lys 180	Ser	Thr	Val	Leu	Ala 185	Ser	Val	Gln	Arg	Gly	Ile	Ala
Glu	Glu	Gln 195	Met	Glu	Asn	Glu	Pro 200	Gln	Phe	Ser	Ala	Ile 205	Met	Gln	Ala
Phe 210	Gly	Gln	Ser	Phe	Leu	Gln 215	Pro	Asp	Ile	His	Leu 220	Phe	Lys	Gln	Asn
Leu 225	Phe	Tyr	Leu	Glu	Thr 230	Leu	Asn	Thr	Lys	Gln 235	Lys	Leu	Tyr	His	Lys 240
Lys	Ile	Phe	Arg	Thr 245	Ala	Met	Leu	Phe	Gln 250	Phe	Val	Asn	Val	Leu 255	Leu
Gln	Val	Leu 260	Val	His	Lys	Ser	His	Asp 265	Leu	Leu	Gln	Glu	Glu	Ile	Gly
Ile	Ala	Ile 275	Tyr	Asn	Met	Ala	Ser 280	Val	Asp	Phe	Asp	Gly	Phe	Phe	Ala
Ala 290	Phe	Leu	Pro	Glu	Phe	Leu 295	Thr	Ser	Cys	Asp	Gly 300	Val	Asp	Ala	Asn
Gln 305	Lys	Ser	Val	Leu	Gly 310	Arg	Asn	Phe	Lys	Met 315	Asp	Arg	Asp	Leu	Pro 320
Ser	Phe	Thr	Gln	Asn 325	Val	His	Arg	Leu	Val 330	Asn	Asp	Leu	Arg	Tyr 335	Tyr
Arg	Leu	Cys	Asn 340	Asp	Ser	Leu	Pro	Pro 345	Gly	Thr	Val	Lys	Leu 350		

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ANTGTCTTGA CTACAAGCTC CACGGGGGC

29

- (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TNGCCAAGGA GAAAGCGAGG CAGACAAGG

29

- (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANATCGACTC TTTGCATCGC ACATTTTGT

29

- (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CNTTCTTCGG ACTTATGTTT GAATCTATC

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CNTTCCTCTT AGATCTCAGT ATCCACCTC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CNCAGACAGG GGAGATAACA ATGAGGTGC

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TNCTATAGGT GACTTCACCC TGTCAGGAG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TNTTACAGGA GCAGGACGCG AGCAGAGAG

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ANTCAGTTGT GGAGGAGGAA ACTGAGGCA

29

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNTCGAAACA GAGTGAGGAA GAAGCTCAG

29

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Val	Ala	Trp	Arg	Ser	Ala	Phe	Leu	Val	Cys	Leu	Ala	Phe	Ser	Leu	
1				5				10						15		
Ala	Thr	Leu	Val	Gln	Arg	Gly	Ser	Gly	Asp	Phe	Asp	Asp	Phe	Asn	Leu	
		20					25						30			
Glu	Asp	Ala	Val	Lys	Glu	Thr	Ser	Ser	Val	Lys	Gln	Pro	Trp	Asp	His	
	35					40					45					
Thr	Thr	Thr	Thr	Thr	Thr	Asn	Arg	Pro	Gly	Thr	Thr	Arg	Ala	Pro	Ala	
	50					55					60					
Lys	Pro	Pro	Gly	Ser	Gly	Leu	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Gln	
65				70					75						80	
Asp	Asp	Gly	Arg	Arg	Lys	Pro	Gly	Ile	Gly	Gly	Arg	Glu	Arg	Trp	Asn	
			85					90						95		
His	Val	Thr	Thr	Thr	Thr	Lys	Arg	Pro	Val	Thr	Thr	Arg	Ala	Pro	Ala	
		100						105					110			
Asn	Thr	Leu	Gly	Asn	Asp	Phe	Asp	Leu	Ala	Asp	Ala	Leu	Asp	Asp	Arg	
		115					120						125			
Asn	Asp	Arg	Asp	Asp	Gly	Arg	Arg	Lys	Pro	Ile	Ala	Gly	Gly	Gly	Gly	
	130					135					140					
Phe	Ser	Asp	Lys	Asp	Leu	Glu	Asp	Ile	Val	Gly	Gly	Gly	Glu	Tyr	Lys	
145					150				155						160	
Pro	Asp	Lys	Gly	Lys	Gly	Asp	Gly	Arg	Tyr	Gly	Ser	Asn	Asp	Asp	Pro	
			165					170						175		
Gly	Ser	Gly	Met	Val	Ala	Glu	Pro	Gly	Thr	Ile	Ala	Gly	Val	Ala	Ser	
		180						185					190			
Ala	Leu	Ala	Met	Ala	Leu	Ile	Gly	Ala	Val	Ser	Ser	Tyr	Ile	Ser	Tyr	
	195					200						205				
Gln	Gln	Lys	Lys	Phe	Cys	Phe	Ser	Ile	Gln	Gln	Gly	Leu	Asn	Ala	Asp	
	210					215					220					

Tyr Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln
 225 230 235 240
 Val Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro
 245 250 255
 Pro Glu Pro Ala Arg Ile
 260

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met His Val Leu Glu Thr Leu Asp Leu Leu Val Leu Arg Ala Asp Lys
 1 5 10 15
 Gly Lys Asp Ala Arg Leu Phe Val Phe Arg Leu Ser Ala Leu Gln Lys
 20 25 30
 Gly Leu Glu Gly Lys Gln Ala Gly Lys Ser Arg Ser Asp Cys Arg Glu
 35 40 45
 Asn Lys Leu Glu Lys Thr Lys Gly Cys His Leu Tyr Ala Ile Asn Thr
 50 55 60
 His His Ser Arg Glu Leu Arg Ile Val Val Ala Ile Arg Asn Lys Leu
 65 70 75 80
 Leu Leu Ile Thr Arg Lys His Asn Lys Pro Ser Gly Val Thr Ser Thr
 85 90 95
 Ser Leu Leu Ser Pro Leu Ser Glu Ser Pro Val Glu Glu Phe Gln Tyr
 100 105 110
 Ile Arg Glu Ile Cys Leu Ser Asp Ser Pro Met Val Met Thr Leu Val
 115 120 125
 Asp Gly Pro Ala Glu Glu Ser Asp Asn Leu Ile Cys Val Ala Tyr Arg
 130 135 140
 His Gln Phe Asp Val Val Asn Glu Ser Thr Gly Glu Ala Phe Arg Leu
 145 150 155 160
 His His Val Glu Ala Asn Arg Val Asn Phe Val Ala Ala Ile Asp Val
 165 170 175
 Tyr Glu Asp Gly Glu Ala Gly Leu Leu Leu Cys Tyr Asn Tyr Ser Cys
 180 185 190

Ile Tyr Lys Lys Val Cys Pro Phe Asn Gly Gly Ser Phe Leu Val Gln
 195 200 205
 Pro Ser Ala Ser Asp Phe Gln Phe Cys Trp Asn Gln Ala Pro Tyr Ala
 210 215 220
 Ile Val Cys Ala Phe Pro Tyr Leu Leu Ala Phe Thr Thr Asp Ser Met
 225 230 235 240
 Glu Ile Arg Leu Val Val Asn Gly Asn Leu Val His Thr Ala Val Val
 245 250 255
 Pro Gln Leu Gln Leu Val Ala Ser Arg Ser Asp Ile Tyr Phe Thr Ala
 260 265 270
 Thr Ala Ala Val Asn Glu Val Ser Ser Gly Gly Ser Ser Lys Gly Ala
 275 280 285
 Ser Ala Arg Asn Ser Pro Gln Thr Pro Pro Gly Arg Asp Thr Pro Val
 290 295 300
 Phe Pro Ser Ser Leu Gly Glu Gly Glu Ile Gln Ser Lys Asn Leu Tyr
 305 310 315 320
 Lys Ile Pro Leu Arg Asn Leu Val Gly Arg Ser Ile Glu Arg Pro Leu
 325 330 335
 Lys Ser Pro Leu Val Ser Lys Val Ile Thr Pro Pro Thr Pro Ile Ser
 340 345 350
 Val Gly Leu Ala Ala Ile Pro Val Thr His Ser Leu Ser Leu Ser Arg
 355 360 365
 Met Glu Ile Lys Glu Ile Ala Ser Arg Thr Arg Arg Glu Leu Leu Gly
 370 375 380
 Leu Ser Asp Glu Gly Gly Pro Lys Ser Glu Gly Ala Pro Lys Ala Lys
 385 390 395 400
 Ser Lys Pro Arg Lys Arg Leu Glu Glu Ser Gln Gly Gly Pro Lys Pro
 405 410 415
 Gly Ala Val Arg Ser Ser Ser Ser Asp Arg Ile Pro Ser Gly Ser Leu
 420 425 430
 Glu Ser Ala Ser Thr Ser Glu Ala Asn Pro Glu Gly His Ser Ala Ser
 435 440 445
 Ser Asp Gln Asp Pro Val Ala Asp Arg Glu Gly Ser Pro Val Ser Gly
 450 455 460
 Ser Ser Pro Phe Gln Leu Thr Ala Phe Ser Asp Glu Asp Ile Ile Asp
 465 470 475 480
 Leu Lys

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTTTAGTGAT	ACGACACAAG	ATCGGGAGAT	TTTTGATCAC	CATACTGAAG	AGGATATAGA	60
TAAAAGTGCT	AACAGTGTAT	TGATAAAAAA	CCTGAGCAGG	ACCCCATCTA	GTTGCAGCAG	120
CTCTCTGGAT	TCAATCAAGG	CTGATGGGAC	CTCTCTGGAC	TTCAGCACTT	ACCGCAGTAG	180
TCAAATGGAA	TCACAGTTTC	TCAGAGATAC	TATTTGTGAA	GAGAGCTTGA	GGGAGAAACT	240
CCAAGATGGG	AGAATAACAA	TAAGGGAGTT	CTTTATACTT	CTCCAGGTCC	ACATCTTGAT	300
ACAGAAACCC	CGACAGAGCA	ATCTCCCAGG	CAATTTTACT	GTAAACACAC	CACCTACTCC	360
AGAAGACCTG	ATGTTAAGTC	AATATGTTTA	CCGACCCAAG	ATACAGATTT	ATAGAGAAGA	420
TTGTGAGGCT	CGTCGCCAAA	AGATTGAAGA	ATTAAAGCTT	TCTGCATCGA	ACCAAGATAA	480
GCTGTTGGTT	GATATAAATA	AGAACCCTGTG	GGAAAAAATG	AGACACTGCT	CTGACAAAGA	540
GCTGAAGGCC	TTTGGAATTT	ATCTTAACAA	AATAAAGTCA	TGTTTTACCA	AGATGACTAA	600
AGTCTTCACT	CACCAAGGAA	AAGTGGCTCT	GTATGGCAAG	CTGGTGCAGT	CAGCTCAGAA	660
TGAGAGGGAG	AAACTTCAAA	TAAAGATAGA	TGAGATGGAT	AAAATACTTA	AGAAGATCGA	720
TAAGTGCTC	ACTGAGATGG	AAACAGAAAC	TAAGAATTTG	GAGGATGAAG	AGAAAAACAA	780
TCCTGTGGAA	GAATGGGATT	CTGAAATGAG	AGCTGCAGAA	AAAGAATTGG	AACAGCTGAA	840
AACTGAAGAG	GAGGAGCTTC	AAAGAAATCT	CTTAGAACTG	GAGGTACCAA	AAGAGCAGAC	900
CCTTGCTCAA	ATAGACTTTA	TGCAAAAACA	AAGAAATAGA	ACTGAAGAGC	TACTGGATCA	960
GTTGAGCTTG	TCTGAGTGGG	ATGTCGTTGA	GTGGAGTGAT	GATCAAGCTG	TATTCACCTT	1020
TGTTTATGAC	ACGATACAAC	TCACCATCAC	CTTTGAAGAG	TCAGTTGTTG	GTTTCCCTTT	1080
CCTGGACAAG	CGTTATAGGA	AGATTGTTGA	TGTCAATTTT	CAATCTCTGT	TAGATGAGGA	1140
TCAAGCTCCT	CCTTCCTCCC	TTTAGTTTCA	TAAGCTTATT	TTCCAGTACG	TTGAAGAAAA	1200
GGAATCCTGG	AAGAAGACAT	GTACAACCCA	GCATCAGTTA	CCCAAGATGC	TTGAAGAATT	1260
CTCACTGGTA	GTGCACCATT	GCAGACTCCT	TGGAGAGGAG	ATTGAGTATT	TAAAGAGATG	1320

GGGACCAAAT TATAACCTAA TGAACATAGA TATTAATAAT AATGAATTGA GACTTTTATT 1380
 CTCTAGCTCC GCAGCATTTG CAAAGTTTGA AATAACTTTG TTTCTCTCAG CCTATTATCC 1440
 ATCTGTACCA TTACCTTCCA CCATTTCAGAA TCACGTTGGG AACACTAGCC AAGATGATAT 1500
 TGCTACCATT CTATCTAAAG TGCCACTGGA GAACAACCTAC CTGAAGAATG TAGTCAAGCA 1560
 AATTTACCAA GATCTGTTTC AGGACTGCCA TTTCTACCAC TAGACCCTTG GACCACCATT 1620
 GGAACAACCA AGCAGAATGT ACTTGATATT ATTTTCAGGGT CCCATTGCTG TTCAGCCTTT 1680
 GTTTTTACGT CATTACAAGC TGAGTAAAAT TCCTTCTGAT GATGTTATAA AAAAAAAAAA 1740
 AAAAAAAAAA 1748

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Glu	Ser	Gln	Phe	Leu	Arg	Asp	Thr	Ile	Cys	Glu	Glu	Ser	Leu	Arg	1	5	10	15
Glu	Lys	Leu	Gln	Asp	Gly	Arg	Ile	Thr	Ile	Arg	Glu	Phe	Phe	Ile	Leu	20	25	30	
Leu	Gln	Val	His	Ile	Leu	Ile	Gln	Lys	Pro	Arg	Gln	Ser	Asn	Leu	Pro	35	40	45	
Gly	Asn	Phe	Thr	Val	Asn	Thr	Pro	Pro	Thr	Pro	Glu	Asp	Leu	Met	Leu	50	55	60	
Ser	Gln	Tyr	Val	Tyr	Arg	Pro	Lys	Ile	Gln	Ile	Tyr	Arg	Glu	Asp	Cys	65	70	75	80
Glu	Ala	Arg	Arg	Gln	Lys	Ile	Glu	Glu	Leu	Lys	Leu	Ser	Ala	Ser	Asn	85	90	95	
Gln	Asp	Lys	Leu	Leu	Val	Asp	Ile	Asn	Lys	Asn	Leu	Trp	Glu	Lys	Met	100	105	110	
Arg	His	Cys	Ser	Asp	Lys	Glu	Leu	Lys	Ala	Phe	Gly	Ile	Tyr	Leu	Asn	115	120	125	
Lys	Ile	Lys	Ser	Cys	Phe	Thr	Lys	Met	Thr	Lys	Val	Phe	Thr	His	Gln	130	135	140	
Gly	Lys	Val	Ala	Leu	Tyr	Gly	Lys	Leu	Val	Gln	Ser	Ala	Gln	Asn	Glu	145	150	155	160

Arg Glu Lys Leu Gln Ile Lys Ile Asp Glu Met Asp Lys Ile Leu Lys
 165 170 175
 Lys Ile Asp Asn Cys Leu Thr Glu Met Glu Thr Glu Thr Lys Asn Leu
 180 185 190
 Glu Asp Glu Glu Lys Asn Asn Pro Val Glu Glu Trp Asp Ser Glu Met
 195 200 205
 Arg Ala Ala Glu Lys Glu Leu Glu Gln Leu Lys Thr Glu Glu Glu Glu
 210 215 220
 Leu Gln Arg Asn Leu Leu Glu Leu Glu Val Pro Lys Glu Gln Thr Leu
 225 230 235 240
 Ala Gln Ile Asp Phe Met Gln Lys Gln Arg Asn Arg Thr Glu Glu Leu
 245 250 255
 Leu Asp Gln Leu Ser Leu Ser Glu Trp Asp Val Val Glu Trp Ser Asp
 260 265 270
 Asp Gln Ala Val Phe Thr Phe Val Tyr Asp Thr Ile Gln Leu Thr Ile
 275 280 285
 Thr Phe Glu Glu Ser Val Val Gly Phe Pro Phe Leu Asp Lys Arg Tyr
 290 295 300
 Arg Lys Ile Val Asp Val Asn Phe Gln Ser Leu Leu Asp Glu Asp Gln
 305 310 315 320
 Ala Pro Pro Ser Ser Leu Leu Val His Lys Leu Ile Phe Gln Tyr Val
 325 330 335
 Glu Glu Lys Glu Ser Trp Lys Lys Thr Cys Thr Thr Gln His Gln Leu
 340 345 350
 Pro Lys Met Leu Glu Glu Phe Ser Leu Val Val His His Cys Arg Leu
 355 360 365
 Leu Gly Glu Glu Ile Glu Tyr Leu Lys Arg Trp Gly Pro Asn Tyr Asn
 370 375 380
 Leu Met Asn Ile Asp Ile Asn Asn Asn Glu Leu Arg Leu Leu Phe Ser
 385 390 395 400
 Ser Ser Ala Ala Phe Ala Lys Phe Glu Ile Thr Leu Phe Leu Ser Ala
 405 410 415
 Tyr Tyr Pro Ser Val Pro Leu Pro Ser Thr Ile Gln Asn His Val Gly
 420 425 430
 Asn Thr Ser Gln Asp Asp Ile Ala Thr Ile Leu Ser Lys Val Pro Leu
 435 440 445
 Glu Asn Asn Tyr Leu Lys Asn Val Val Lys Gln Ile Tyr Gln Asp Leu
 450 455 460

Phe Gln Asp Cys His Phe Tyr His
465 470

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTTTCTTTG ATTGTCTCTG CTTTAGCGTC TCTAAATCCG GTCACCATGT CGGACCCCGA	60
AGGCGAGACC TTGCGAAGCA CCTTTCCTC TTATATGGCC GAAGGCGAGC GGCTCTACCT	120
GTGCGGGGAA TTTTCTAAAG CCGCGCAGAG CTTCAGCAAC GCTCTTTACC TTCAGGATGG	180
AGACAAGAAC TGCCTGGTTG CTCGCTCAA GTGCTTCCTG AAGATGGGAG ACTTGAGAG	240
ATCCCTGAAG GATGCTGARG CTTCGCTCCA GAGTGACCCA GCTTTCTGTA AGGGGATTTT	300
GCAAAAGGCT GAGACACTGT ACACCATGGG AGACTTTGAG TTTGCCTTGG TATTCTATCA	360
TCGARGCTAC AAGCTGARGC CTGATCGGGA ATTCARARTT GGCATTCAGA AAGCCCAGGA	420
AGCCATCAAC AACTCAGTGG GAAGTCCTTC TTCCATTAAG CTGGAGAACA AAGGGGACCT	480
CTCCTTCTTA AGCAAGCAGG CTGAGAATAT AAAAGCCCAG CAGAAGCCTC AGCCCATGAA	540
ACACCTCTTA CACCCACCA AGGGAGAGCC CAAGTGGAAG GCCTCGCTCA AGAGTGAGAA	600
GACTGTCCGC CAGCTTCTGG GGGAGCTCTA CGTGGACAAA GAGTATTTGG AGAAGCTCCT	660
ATTGGATGAA GACCTGATCA AAGGCACCAT GAAGGGCGGC CTGACTGTGG AGGACCTCAT	720
CATGACGGGC ATCAACTACC TGGATACTCA CAGCAACTTC TGGAGGCAGC AGAAGCCGAT	780
CTACGCCAGG GAGCGGGACC GGAAGCTGAT GCAAGAGAAA TGGCTGCGGG ACCACAAACG	840
CCGTCCCTCA CAGACAGCCC ATTACATCCT CAAGAGCCTG GAGGACATTG ATATGTTGCT	900
CACAAGTGGC AGTGCTGAAG GGAGTCTTCA GAAAGCTGAG AAAGTGCTGA AGAAGGTACT	960
GGAATGGAAC AAGGAAGAGG TACCCAACAA GGATGAACTG GTTGGAAACT TGTATAGCTG	1020
CATAGGGAAT GCCCAGATTG AGCTGGGGCA GATGGAGGCA GCCCTGCAGA GCCACAGAAA	1080
GGACYTGGAG ATCGCCAAGG AATATGACCT TCCTGATGCA AAATCGAGAG CCCTTGACAA	1140
CATTGGCAGA GTTTTTGCCA GAGTTGGGAA ATTCCAGCAA GCCATTGACA CGTGGGAAGA	1200
AAAGATCCCT CTGGCAAAAA CCACCCTGGA GAAGACCTGG CTGTTCCACG AGATCGGCCG	1260

CTGCTACTTG GAGCTGGACC AGGCCTGGCA GGCCCAGAAT TATGGCGAGA AGTCCCAGCA 1320
 GTGTGCCGAG GAGGAAGGGG ACATTGAGTG GCAACTGAAT GCCAGTGTTT TGGTGGCCCA 1380
 GGCACAAGTG AAGCTGAGAG ACTTCGAGTC AGCCGTGAAC AATTTTGAGA AGGCCCTGGA 1440
 GAGAGCAAAG CTTGTGCATA ACAACGAGGC GCAGCAGGCC ATCATCAGTG CCTTGGACGA 1500
 TGCCAACAAG GGTATCATCA GAGAACTGAG GAAAACCAAC TACGTGGAGA ATCTCAAAGA 1560
 AAAAAGCGAG GGAGAAGCTT CACTGTATGA AGATAGAATA ATAACAAGAG AGAAGGACAT 1620
 GAGGAGAGTG AGAGATGAGC CCGAGAAGGT GGTGAAGCAG TGGGACCATA GTGAGGATGA 1680
 GAAAGAGACA GATGAGGACG ATGAGGCTTT TGGGGAAGCT CTGCAGAGCC CAGCAAGCGG 1740
 AAAGCAGAGT GTGGAAGCAG GAAAAGCCAG AAGCGATTTG GGAGCAGTTG CCAAGGGCCT 1800
 GTCAGGAGAA TTAGGCACAA GATCAGGAGA AACAGGCAGG AAGCTACTAG AAGCTGGCAG 1860
 AAGAGAGTCA AGAGAAATTT ATAGGAGGCC TTCGGGAGAA TTAGAGCAAA GACTCTCAGG 1920
 AGAATTCAGC AGACAGGAAC CAGAAGAACT AAAGAACTT TCAGAAGTGG GCAGAAGAGA 1980
 SCCAGAAGAA YTGGAAGAAA CACAATTTGG AGAAATAGGA GAAACGAAAA AAACAGGAAA 2040
 TGAGATGGAA AAGGAATATG AATGAAGCCA TCGGTAGAGA TGAGGATCAG GAAGCTGGTG 2100
 TTCAGAGGGA TCATGGGATT TTATTAACT GGATTTTCAA GCGATTTGTC TGTTATAGGA 2160
 AAAATGAGGG TTTTACTTYT GCTGCTTCC ATCACTATTT TGCCATTAAA TAGGTGTCTT 2220
 TCACTCTTGC MAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2280
 AAAAAAAAAA AAAAAAAAAA 2298

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Ser Asp Pro Glu Gly Glu Thr Leu Arg Ser Thr Phe Pro Ser Tyr
 1 5 10 15

Met Ala Glu Gly Glu Arg Leu Tyr Leu Cys Gly Glu Phe Ser Lys Ala
 20 25 30

Ala Gln Ser Phe Ser Asn Ala Leu Tyr Leu Gln Asp Gly Asp Lys Asn
 35 40 45

Cys Leu Val Ala Arg Ser Lys Cys Phe Leu Lys Met Gly Asp Leu Glu

50	55	60
Arg Ser Leu Lys Asp	Ala Glu Ala Ser Leu Gln Ser Asp Pro Ala Phe	
65	70	75 80
Cys Lys Gly Ile Leu Gln Lys Ala Glu Thr Leu Tyr Thr Met Gly Asp		
	85 90 95	
Phe Glu Phe Ala Leu Val Phe Tyr His Arg Xaa Tyr Lys Leu Xaa Pro		
	100 105 110	
Asp Arg Glu Phe Xaa Xaa Gly Ile Gln Lys Ala Gln Glu Ala Ile Asn		
	115 120 125	
Asn Ser Val Gly Ser Pro Ser Ser Ile Lys Leu Glu Asn Lys Gly Asp		
	130 135 140	
Leu Ser Phe Leu Ser Lys Gln Ala Glu Asn Ile Lys Ala Gln Gln Lys		
145	150 155	160
Pro Gln Pro Met Lys His Leu Leu His Pro Thr Lys Gly Glu Pro Lys		
	165 170 175	
Trp Lys Ala Ser Leu Lys Ser Glu Lys Thr Val Arg Gln Leu Leu Gly		
	180 185 190	
Glu Leu Tyr Val Asp Lys Glu Tyr Leu Glu Lys Leu Leu Leu Asp Glu		
	195 200 205	
Asp Leu Ile Lys Gly Thr Met Lys Gly Gly Leu Thr Val Glu Asp Leu		
	210 215 220	
Ile Met Thr Gly Ile Asn Tyr Leu Asp Thr His Ser Asn Phe Trp Arg		
225	230 235	240
Gln Gln Lys Pro Ile Tyr Ala Arg Glu Arg Asp Arg Lys Leu Met Gln		
	245 250 255	
Glu Lys Trp Leu Arg Asp His Lys Arg Arg Pro Ser Gln Thr Ala His		
	260 265 270	
Tyr Ile Leu Lys Ser Leu Glu Asp Ile Asp Met Leu Leu Thr Ser Gly		
	275 280 285	
Ser Ala Glu Gly Ser Leu Gln Lys Ala Glu Lys Val Leu Lys Lys Val		
	290 295 300	
Leu Glu Trp Asn Lys Glu Glu Val Pro Asn Lys Asp Glu Leu Val Gly		
305	310 315	320
Asn Leu Tyr Ser Cys Ile Gly Asn Ala Gln Ile Glu Leu Gly Gln Met		
	325 330 335	
Glu Ala Ala Leu Gln Ser His Arg Lys Asp Leu Glu Ile Ala Lys Glu		
	340 345 350	
Tyr Asp Leu Pro Asp Ala Lys Ser Arg Ala Leu Asp Asn Ile Gly Arg		
	355 360 365	

Val	Phe	Ala	Arg	Val	Gly	Lys	Phe	Gln	Gln	Ala	Ile	Asp	Thr	Trp	Glu	
370						375					380					
Glu	Lys	Ile	Pro	Leu	Ala	Lys	Thr	Thr	Leu	Glu	Lys	Thr	Trp	Leu	Phe	
385					390					395					400	
His	Glu	Ile	Gly	Arg	Cys	Tyr	Leu	Glu	Leu	Asp	Gln	Ala	Trp	Gln	Ala	
				405					410					415		
Gln	Asn	Tyr	Gly	Glu	Lys	Ser	Gln	Gln	Cys	Ala	Glu	Glu	Glu	Gly	Asp	
			420					425					430			
Ile	Glu	Trp	Gln	Leu	Asn	Ala	Ser	Val	Leu	Val	Ala	Gln	Ala	Gln	Val	
		435					440					445				
Lys	Leu	Arg	Asp	Phe	Glu	Ser	Ala	Val	Asn	Asn	Phe	Glu	Lys	Ala	Leu	
	450					455					460					
Glu	Arg	Ala	Lys	Leu	Val	His	Asn	Asn	Glu	Ala	Gln	Gln	Ala	Ile	Ile	
465					470					475					480	
Ser	Ala	Leu	Asp	Asp	Ala	Asn	Lys	Gly	Ile	Ile	Arg	Glu	Leu	Arg	Lys	
				485					490					495		
Thr	Asn	Tyr	Val	Glu	Asn	Leu	Lys	Glu	Lys	Ser	Glu	Gly	Glu	Ala	Ser	
			500					505					510			
Leu	Tyr	Glu	Asp	Arg	Ile	Ile	Thr	Arg	Glu	Lys	Asp	Met	Arg	Arg	Val	
		515					520					525				
Arg	Asp	Glu	Pro	Glu	Lys	Val	Val	Lys	Gln	Trp	Asp	His	Ser	Glu	Asp	
	530					535					540					
Glu	Lys	Glu	Thr	Asp	Glu	Asp	Asp	Glu	Ala	Phe	Gly	Glu	Ala	Leu	Gln	
545					550					555					560	
Ser	Pro	Ala	Ser	Gly	Lys	Gln	Ser	Val	Glu	Ala	Gly	Lys	Ala	Arg	Ser	
				565					570					575		
Asp	Leu	Gly	Ala	Val	Ala	Lys	Gly	Leu	Ser	Gly	Glu	Leu	Gly	Thr	Arg	
			580					585					590			
Ser	Gly	Glu	Thr	Gly	Arg	Lys	Leu	Leu	Glu	Ala	Gly	Arg	Arg	Glu	Ser	
		595					600					605				
Arg	Glu	Ile	Tyr	Arg	Arg	Pro	Ser	Gly	Glu	Leu	Glu	Gln	Arg	Leu	Ser	
	610					615					620					
Gly	Glu	Phe	Ser	Arg	Gln	Glu	Pro	Glu	Glu	Leu	Lys	Lys	Leu	Ser	Glu	
625					630					635					640	
Val	Gly	Arg	Arg	Xaa	Pro	Glu	Glu	Leu	Gly	Lys	Thr	Gln	Phe	Gly	Glu	
				645					650					655		
Ile	Gly	Glu	Thr	Lys	Lys	Thr	Gly	Asn	Glu	Met	Glu	Lys	Glu	Tyr	Glu	
			660					665					670			

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGAAGAGCCA CCATCCCTGC CCCCGTTTTTC CCACCGGGGA GTCTGTACAG AGATTTTTTCT	60
ACGTTTTTAT TTTTTCCTC AGAGGGATGG GATTGGGGAG GAGGGGATGG GCAGCGGAGG	120
GTTGGGGGCA TGGTCTGCAG GCTCATCTGT GTCCGCCTTT CACTCCACTA ATGCTGTCTC	180
AGTGTCTTCT CTCTCTCTCT TTCGAGCTTG CACTCCGGTA CCCGACCCGG CGCCCTGGCC	240
CATCCCATGC CGGGGGGCCA GTGGAAAGAA GACAGGCCGT CCAGCCCGTG CCCGCCTGCG	300
GCGGGGGCAC CCAGCAAGCC CGCCCACCGC CCGCTGCCTC ACCTGCTTCG CCACAGACTC	360
TTGTTCCCAG CCCCTTGGGG CCTCCGTGTT TGGGGTGGGG GAGCTGCTTA GAGACTGTGC	420
CCGTCTCGG CCCCCACCC TGAAGTGCCA GCACCACCAG CACCAGATCT TCCGCCGCCA	480
CACCGCATTG AGGACACGCC GGCCGGGCCG CTTCGTCTCA AGTTGTATAA AGTTGTCTCC	540
GTGTCCCCTC CTCCCTCTGC CCCAGTGTT TCTTCTGATT TTTTTTCCC CTTTCCCTCC	600
CTCCCTCTCC GCATTCTTCC CTTGGTTCAG CACAGGTAAA ACGGTTCCCC TCCCTCCCTG	660
CCTTCATGGA TCACCAGCTC ACGTCATGTT GCCTTCTCTT TTCTTTGTGT GTGTGTTTAT	720
TTAAGTTATT TTTCTTCCTC CTCTCCCTTT TCTTTTGGC CCTCCCTCCC TCCCTCTTCT	780
GCCATGTAAC TGGAGGATGT GCTATGAGTT TGCAAACAGC TGGACTGTCA GGCTGCTTTT	840
TTTTCCAGAT GTTCTTCTTC TGCTTCCCCT TCCCCTCCTC TCCCCTCCTT TTCCTTCTT	900
CCTTCCTTTC CTTGGAGCAC TGAGCACCAT TTGGAAGCTT GAGAGAAACC AAAATTAAAG	960
AGAGAAAGAG AGAGCGTGCA CGCTCCTGCT TTGTCAAAAA AAAAAAAAAA	1010

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Gly	Ser	Gly	Gly	Leu	Gly	Ala	Trp	Ser	Ala	Gly	Ser	Ser	Val	Ser	
1				5					10					15		
Ala	Phe	His	Ser	Thr	Asn	Ala	Val	Ser	Val	Phe	Ser	Leu	Ser	Leu	Phe	
			20					25					30			
Arg	Ala	Cys	Thr	Pro	Val	Pro	Asp	Pro	Ala	Pro	Trp	Pro	Ile	Pro	Cys	
		35					40					45				
Arg	Gly	Ala	Ser	Gly	Lys	Lys	Thr	Gly	Arg	Pro	Ala	Arg	Ala	Arg	Leu	
	50					55					60					
Arg	Arg	Gly	His	Pro	Ala	Ser	Pro	Pro	Thr	Ala	Arg	Cys	Leu	Thr	Cys	
65					70					75				80		
Phe	Ala	Thr	Asp	Ser	Cys	Ser	Gln	Pro	Leu	Gly	Ala	Ser	Val	Phe	Gly	
			85						90					95		
Val	Gly	Glu	Leu	Leu	Arg	Asp	Cys	Ala	Arg	Pro	Arg	Pro	Pro	Thr	Leu	
			100					105					110			
Lys	Cys	Gln	His	His	Gln	His	Gln	Ile	Phe	Arg	Arg	His	Thr	Ala	Leu	
		115					120					125				
Arg	Thr	Arg	Arg	Pro	Gly	Arg	Phe	Val	Ser	Ser	Cys	Ile	Lys	Leu	Ser	
	130					135					140					
Pro	Cys	Pro	Leu	Leu	Pro	Leu	Pro	Pro	Val	Phe	Leu	Leu	Ile	Phe	Phe	
145					150					155					160	
Ser	Pro	Phe	Pro	Pro	Ser	Leu	Ser	Ala	Phe	Phe	Pro	Trp	Phe	Ser	Thr	
					165				170					175		
Gly	Lys	Thr	Val	Pro	Leu	Pro	Pro	Cys	Leu	His	Gly	Ser	Pro	Ala	His	
			180					185					190			
Val	Met	Leu	Pro	Ser	Leu	Phe	Phe	Val	Cys	Val	Phe	Ile				
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTTYGCTCA TCAACCTCAT TATAGAACAT ATGATTGTG ATACAGATCC TGAAGTTGGA	60
GGAGCAGTCC AGCTTATGGG CCTGCTTCGA ACTTTAGTTG ACCCAGAGAA CATGCTAGCC	120
ACTGCCMATA AAACASAAAA GACTGAATTT CTGGGTTTCT TCTACAAGCA CTGTATGCAT	180

GTTCTCWCTG	CTCCTTTACT	AGCAAATACA	ACAGAAGACA	AACCTAGTAA	AGATGATTTT	240
CAGACTGCCC	AACTATTGGC	ACTTGTATTG	GAATTGTAA	CATTTTGTGT	GGAGCACCAT	300
ACCTACCACA	TAAAGAACTA	CATTATTAAT	AAGGATATCC	TCCGGAGAGT	GCTAGTTCTT	360
ATGGCCTCGA	AGCATGCTTT	CTTGGCATT	TGTGCCCTTC	GTTTTAAAAG	AAAGATTATT	420
GGATTAAAAG	ATGAGTTTTA	CAACCGCTAC	ATAATGAAAA	GTTTTTTTGT	TGAACCAGTA	480
GTGAAAGCAT	TTCTCAACAA	TGGATCCCGC	TACAATCTGA	TGAACTCTGC	CATAATAGAG	540
ATGTTTGAAT	TTATTAGAGT	GGAAGATATA	AAATCATTAA	CTGCTCATGT	AATTGAAAAT	600
TACTGGAAAG	CACTGGAAGA	TGTAGATTAT	GTACAGACAT	TTAAAGGATT	AAAAGTGA	660
TTTGAACAAC	AAAGAGAAAG	GCAAGATAAT	CCCAAACCTG	ACAGTATGCG	TTCCATTTTG	720
AGGAATCACA	GATATCGAAG	AGATGCCAGA	ACACTAGAAG	ATGAAGAAGA	GATGTGGTTT	780
AACACAGATG	AAGATGACAT	GGAAGATGGA	GAAGCTGTAG	TGTCTCCATC	TGACAAAAC	840
AAAAATGATG	ATGATATTAT	GGATCCAATA	AGTAAATTCA	TGGAAAGGAA	GAAATTAATA	900
GAAAGTGAGG	AAAAGGAAGT	GCTTCTGAAA	ACAAACCTTT	CTGGACGGCA	GAGCCCAAGT	960
TTCAAGCTTT	CCCTGTCCAG	TGGAACGAAG	ACTAACCTCA	CCAGCCAGTC	ATCTACAACA	1020
AATCTGCCTG	GTTCTCCGGG	ATCACCTGGA	TCCCCAGGAT	CTCCAGGCTC	TCCTGGATCC	1080
GTACCTAAAA	ATACATCTCA	GACGGCAGCT	ATTACTACAA	AGGGAGGCCT	CGTGGGTCTG	1140
GTAGATTATC	CTGATGATGA	TGAAGATGAT	GATGAGGATG	AAGATAAGGA	AGATACGTTA	1200
CCATTGTCAA	AGAAAGCAAA	ATTTGATTCA	TAATAATGGC	AACGGCCTAG	GATCAGTACC	1260
TGTTGAAAAA	AACTGGTTCT	CCACCCCTCC	CCCATACAAA	ATCCACAAAA	AAGCGCAGTG	1320
GTCTCTTG	AATGACTGAC	ACAGATCAGC	CTCTTACACT	TGACTTCTGC	TCATCAAGTG	1380
CCAATTCAAT	GGAGCAGGAG	GAGGGGATAT	CATATATTTA	GGGGAAAGAC	TTAAGCCTTT	1440
GAGCTCTCCA	GCTTGACCA	CACATTGCCC	TTTTCTCAGG	GAAGGAAATG	GAAACAAAAA	1500
GCCAACAGGG	CAGGGGTTTT	GTAAGTGGAA	CTCTGGATTG	ACTGGTCAGT	TGCTACAATC	1560
AGAATATGCT	TTCTTGGAAC	ATGTTTGAGA	CTCAGAAGAA	TGGCCTTTCT	GCCATAATTC	1620
TTCCTAGTC	AAGAATGCCA	GCAGTTTCTT	TGTATAAAGA	GACCTGCCTT	TAAATCATA	1680
CATTCTGAAC	ATTTTAGTCA	AGCTACAACA	GGTTTGGA	ACCTCTGTGG	GGGAGGGGCG	1740
AGTATAAAGT	TTTCTCTTT	TTTAACTGTT	CCCTTTGCCC	TTCAAACCTGC	AGATATTTTT	1800
TTTTTTAAGT	GGGGACTTCT	CCCTACTTGA	TTAAAGATTG	AGTGGAATTC	TAGATGTGGT	1860

CATTGTGTC ATAATTTTTT TGTTTTATTT TGTTTTTGAT TTTTTTTTTC CTCCCCTGAG 1920
 TGTATGCTTA GTTGTGAGT ATATATATTT GGGACCATTA AAACCTTTTTT TGATGTAATA 1980
 TAACCTAACG TTGTGCTGGT ACCTGTTTTA CCATGTGTAA TTTTGTCTT ACATCACAGT 2040
 TCTTAATTTG TTTAGAGTTT TATGAAAGAT GGTATAGTTT TTATTGACAA AAGCAAAGTA 2100
 ATCTTACAAC TATGTGCATA CAAAAGCAAT ACTATTTTGT GACTAAATAT TTTATATTAA 2160
 AATTTACATC AGCAACTGTC TTGAGAATTC AGGGAAATAG AATGGAATTT AAAACTTCAA 2220
 CAGTTTTGTT AAATCTAGAA ACATGAAATT RGTATTCCAA AGAGATTCTG AAATTTCTTT 2280
 TCTKGGGGAA ATGACGGTAC ATTAAATCAA AATTGRGGAT GGATGATTTA AAAACATTTG 2340
 ACTTTTTAAT AATAAAAAGA AAAGTGAAGA GTAAGAGAAA TTGTAAAAAA AAAAAAAAAA 2400
 AAAAAAAAAA 2409

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Ile	Cys	Asp	Thr	Asp	Pro	Glu	Leu	Gly	Gly	Ala	Val	Gln	Leu	Met
1				5					10					15	
Gly	Leu	Leu	Arg	Thr	Leu	Val	Asp	Pro	Glu	Asn	Met	Leu	Ala	Thr	Ala
			20					25					30		
Xaa	Lys	Thr	Xaa	Lys	Thr	Glu	Phe	Leu	Gly	Phe	Phe	Tyr	Lys	His	Cys
		35					40					45			
Met	His	Val	Leu	Xaa	Ala	Pro	Leu	Leu	Ala	Asn	Thr	Thr	Glu	Asp	Lys
	50					55					60				
Pro	Ser	Lys	Asp	Asp	Phe	Gln	Thr	Ala	Gln	Leu	Leu	Ala	Leu	Val	Leu
65					70					75				80	
Glu	Leu	Leu	Thr	Phe	Cys	Val	Glu	His	His	Thr	Tyr	His	Ile	Lys	Asn
			85						90					95	
Tyr	Ile	Ile	Asn	Lys	Asp	Ile	Leu	Arg	Arg	Val	Leu	Val	Leu	Met	Ala
			100					105					110		
Ser	Lys	His	Ala	Phe	Leu	Ala	Leu	Cys	Ala	Leu	Arg	Phe	Lys	Arg	Lys
			115					120				125			
Ile	Ile	Gly	Leu	Lys	Asp	Glu	Phe	Tyr	Asn	Arg	Tyr	Ile	Met	Lys	Ser

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(i) SEQUENCE CHARACTERISTICS:

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCCAGGCAGG GTGTGGGGGC AGCTGTGCCA ATCTACCTCA CAGGCCACC CCCTGCCGGG 60
CATGCCGTGG GATCATGGGC AGGGAAGGCT CTGGGGGTCG GAGACACCGC TGCTTAGCAC 120
CCCCAGCCAG AACACCCTGA GGTCTCGGG GCTCTGGAGA GAGTGGGGCG GGAGGAAGAA 180
TTGGCACCTT CCTAGGGAAG GAGACGAGCG CTTCGCCTTG ATTCTCCGAG AAGCCTCCGA 240
GAAGTGCTTT AAGTGTGTTT GCATGCSCCA GGCGGTGGGC AGCGGGGGCC TGTCCARCCC 300
TCTCCCGCCA TCCTTCCCCA AGTGACGTCC ACTGCCTTGT CACCAGCGAC CTGCCTGTCA 360
TGCCACCCCC CTGAGGAAGC ATGGGGACCC TAACACCCTG GTGCCCTGCA CCAGACAGGC 420
CGTGGTCAGG CCCAGGCCAC CGGCCGGGTT CTGCCACARC TTCCCACGTG CTTGCTGACA 480
TGCSTGTGCC TGTGTGTGGT GTCTGTTGCT GTGTCGTGAA ACTGTGACCA TCACTCAGTC 540
CAAACAAGTG AGTGGCCCTS GAGGCCACAG TTATGCAACT TTCAGTGTGT GTCATAACGA 600
CGTCAC'TGCT TTTTAAACTC GATAACTCTT TATTTTAGTA AAATGCCAG GAGTCCTGGA 660
AGCTACGCGG ACTTGCAGAG GTTTTATTTT TTGGCCTTAG AATCTGCAGA AATTAGGAGG 720
CACCGAGCCC AGCGCAGCAG CCTCGGACCC GGATTGCGTT TGCCTTAGCG GATATGTTTA 780
TACAGATGAA TATAAAATGT TTTTCTTTT GGGCTTTTGT CTTCTTTTTT CCCCCCTTC 840
TCACCTTCCC TTCTCCCTGA CCCCACCCCC CAAAAAGCT ACTTCTTCAT TCCGTGGTAC 900
GATTATTTTT TTTAACTAAA GGAAGATAAA ATTCTAAAAA AAAAAAAAAA A 951

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Pro Trp Asp His Gly Gln Gly Arg Leu Trp Gly Ser Glu Thr Pro
1 5 10 15
Leu Leu Ser Thr Pro Ser Gln Asn Thr Leu Arg Val Ser Gly Leu Trp
20 25 30
Arg Glu Trp Gly Gly Arg Lys Asn Trp His Leu Pro Arg Glu Gly Asp
35 40 45

Glu Arg Phe Ala Leu Ile Leu Arg Glu Ala Ser Glu Lys Cys Phe Lys
50 55 60

Cys Val Cys Met Xaa Gln Ala Val Gly Ser Gly Gly Leu Ser Xaa Pro
65 70 75 80

Leu Pro Pro Ser Phe Pro Lys
85

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1899 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCCGCTTGT GTCCACGGGA CGCGGGCGGA TCTTCTCCGG CCATGAGGAA GCCAGCCGCT	60
GGCTTCCTTC CCTCACTCCT GAAGGTGCTG CTCCTGCCTC TGGCACCTGC CGCAGCCCAG	120
GATTCGACTC AGGCCTCCAC TCCAGGCAGC CCTCTCTCTC CTACCGAATA CGAACGCTTC	180
TTCGCACTGC TGACTCCAAC CTGGAAGGCA GAGACTACCT GCCGTCTCCG TGCAACCCAC	240
GGCTGCCGGA ATCCCACACT CGTCCAGCTG GACCAATATG AAAACCACGG CTTAGTGCCC	300
GATGGTGCTG TCTGCTCCAA CCTCCCTTAT GCCTCCTGGT TTGAGTCTTT CTGCCAGTTC	360
ACTCACTACC GTTGCTCCAA CCACGTCTAC TATGCCAAGA GAGTCCTGTG TTCCCAGCCA	420
GTCTCTATTC TCTCACCTAA CACTCTCAAG GAGATAGAAG CTTCAGCTGA AGTCTCACCC	480
ACCACGATGA CCTCCCCCAT CTCACCCAC TTCACAGTGA CAGAACGCCA GACCTTCCAG	540
CCCTGGCCTG AGAGGCTCAG CAACAACGTG GAAGAGCTCC TACAATCCTC CTTGTCCCTG	600
GGAGGCCAGG AGCAAGCGCC AGAGCACAAG CAGGAGCAAG GAGTGGAGCA CAGGCAGGAG	660
CCGACACAAG AACACAAGCA GGAAGAGGGG CAGAAACAGG AAGAGCAAGA AGAGGAACAG	720
GAAGAGGAGG GAAAGCAGGA AGAAGGACAG GGGACTAAGG AGGGACGGGA GGCTGTGTCT	780
CAGCTGCAGA CAGACTCAGA GCCCAAGTTT CACTCTGAAT CTCTATCTTC TAACCCTTCC	840
TCTTTTGCTC CCCGGGTACG AGAAGTAGAG TCTACTCCTA TGATAATGGA GAACATCCAG	900
GAGCTCATTC GATCAGCCCA GGAAATAGAT GAAATGAATG AAATATATGA TGAGAACTCC	960
TACTGGAGAA ACCAAAACCC TGGCAGCCTC CTGCAGCTGC CCCACACAGA GGCCTTGCTG	1020
GTGCTGTGCT ATTCGATCGT GGAGAATACC TGCATCATAA CCCCCACAGC CAAGGCCTGG	1080

AAGTACATGG AGGAGGAGAT CCTTG GTTTC GGGAAGTCGG TCTGTGACAG CCTTGGGCGG 1140
 CGACACATGT CTACCTGTGC CCTCTGTGAC TTCTGCTCCT TGAAGCTGGA GCAGTGCCAC 1200
 TCAGAGGCCA GCCTGCAGCG GCAACAATGC GACACCTCCC ACAAGACTCC CTTTGTTCAGC 1260
 CCCTTGCTTG CCTCCCAGAG CCTGTCCATC GGCAACCAGG TAGGGTCCCC AGAATCAGGC 1320
 CGCTTTTACG GGCTGGATTT GTACGGTGGG CTCCACATGG ACTTCTGGTG TGCCCGGCTT 1380
 GCCACGAAAG GCTGTGAAGA TGTCCGAGTC TCTGGGTGGC TCCAGACTGA GTTCCTTAGC 1440
 TTCCAGGATG GGGATTTCCC TACCAAGATT TGTGACACAG ACTATATCCA GTACCCAAAC 1500
 TACTGTTCTT TCAAAAGCCA GCAGTGTCTG ATGAGAAACC GCAATCGGAA GGTGTCCCGC 1560
 ATGAGATGTC TGCAGAAATGA GACTTACAGT GCGCTGAGCC TGGCAAAAGT GAGGACGTTG 1620
 TGCTTTTCGAT GGAGCCAGGA GTTCAGCACC TTGACTCTAG GCCAGTTCGG ATGAGCTKGS 1680
 GTTTATTTTG CCCACACCCC AGCCCAACCT GCCCASGTTC TCTATTGTTT TGAGACCCCA 1740
 TTGCTTTCAG GCTGCCCCCT CTGGGTCTGT TACTCGGCCC CTAMTCACAT TTCCTTGGGT 1800
 TGGAGCAACA GTCCCAGAGA GGGCCACGGT GGGAGCTGCG CCCTCCTTAA AAGATGACTT 1860
 TACATAAAAT GTTGATCTTC AAAAAAAAAA AAAAAAAAAA 1899

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Arg	Lys	Pro	Ala	Ala	Gly	Phe	Leu	Pro	Ser	Leu	Leu	Lys	Val	Leu
1				5					10					15	
Leu	Leu	Pro	Leu	Ala	Pro	Ala	Ala	Ala	Gln	Asp	Ser	Thr	Gln	Ala	Ser
			20					25					30		
Thr	Pro	Gly	Ser	Pro	Leu	Ser	Pro	Thr	Glu	Tyr	Glu	Arg	Phe	Phe	Ala
			35					40					45		
Leu	Leu	Thr	Pro	Thr	Trp	Lys	Ala	Glu	Thr	Thr	Cys	Arg	Leu	Arg	Ala
		50				55					60				
Thr	His	Gly	Cys	Arg	Asn	Pro	Thr	Leu	Val	Gln	Leu	Asp	Gln	Tyr	Glu
65					70					75				80	
Asn	His	Gly	Leu	Val	Pro	Asp	Gly	Ala	Val	Cys	Ser	Asn	Leu	Pro	Tyr
				85					90					95	

Ala	Ser	Trp	Phe	Glu	Ser	Phe	Cys	Gln	Phe	Thr	His	Tyr	Arg	Cys	Ser	
			100					105					110			
Asn	His	Val	Tyr	Tyr	Ala	Lys	Arg	Val	Leu	Cys	Ser	Gln	Pro	Val	Ser	
			115				120					125				
Ile	Leu	Ser	Pro	Asn	Thr	Leu	Lys	Glu	Ile	Glu	Ala	Ser	Ala	Glu	Val	
			130			135					140					
Ser	Pro	Thr	Thr	Met	Thr	Ser	Pro	Ile	Ser	Pro	His	Phe	Thr	Val	Thr	
145					150					155						160
Glu	Arg	Gln	Thr	Phe	Gln	Pro	Trp	Pro	Glu	Arg	Leu	Ser	Asn	Asn	Val	
				165					170							175
Glu	Glu	Leu	Leu	Gln	Ser	Ser	Leu	Ser	Leu	Gly	Gly	Gln	Glu	Gln	Ala	
			180					185					190			
Pro	Glu	His	Lys	Gln	Glu	Gln	Gly	Val	Glu	His	Arg	Gln	Glu	Pro	Thr	
			195					200					205			
Gln	Glu	His	Lys	Gln	Glu	Glu	Gly	Gln	Lys	Gln	Glu	Glu	Gln	Glu	Glu	
			210					215					220			
Glu	Gln	Glu	Glu	Glu	Gly	Lys	Gln	Glu	Glu	Gly	Gln	Gly	Thr	Lys	Glu	
225					230					235						240
Gly	Arg	Glu	Ala	Val	Ser	Gln	Leu	Gln	Thr	Asp	Ser	Glu	Pro	Lys	Phe	
				245					250							255
His	Ser	Glu	Ser	Leu	Ser	Ser	Asn	Pro	Ser	Ser	Phe	Ala	Pro	Arg	Val	
			260					265					270			
Arg	Glu	Val	Glu	Ser	Thr	Pro	Met	Ile	Met	Glu	Asn	Ile	Gln	Glu	Leu	
			275					280					285			
Ile	Arg	Ser	Ala	Gln	Glu	Ile	Asp	Glu	Met	Asn	Glu	Ile	Tyr	Asp	Glu	
			290					295					300			
Asn	Ser	Tyr	Trp	Arg	Asn	Gln	Asn	Pro	Gly	Ser	Leu	Leu	Gln	Leu	Pro	
305					310					315						320
His	Thr	Glu	Ala	Leu	Leu	Val	Leu	Cys	Tyr	Ser	Ile	Val	Glu	Asn	Thr	
				325					330							335
Cys	Ile	Ile	Thr	Pro	Thr	Ala	Lys	Ala	Trp	Lys	Tyr	Met	Glu	Glu	Glu	
			340					345					350			
Ile	Leu	Gly	Phe	Gly	Lys	Ser	Val	Cys	Asp	Ser	Leu	Gly	Arg	Arg	His	
			355					360					365			
Met	Ser	Thr	Cys	Ala	Leu	Cys	Asp	Phe	Cys	Ser	Leu	Lys	Leu	Glu	Gln	
			370					375					380			
Cys	His	Ser	Glu	Ala	Ser	Leu	Gln	Arg	Gln	Gln	Cys	Asp	Thr	Ser	His	
385					390					395						400

Lys Thr Pro Phe Val Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile
405 410 415

Gly Asn Gln Val Gly Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp
420 425 430

Leu Tyr Gly Gly Leu His Met Asp Phe Trp Cys Ala Arg Leu Ala Thr
435 440 445

Lys Gly Cys Glu Asp Val Arg Val Ser Gly Trp Leu Gln Thr Glu Phe
450 455 460

Leu Ser Phe Gln Asp Gly Asp Phe Pro Thr Lys Ile Cys Asp Thr Asp
465 470 475 480

Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser Phe Lys Ser Gln Gln Cys Leu
485 490 495

Met Arg Asn Arg Asn Arg Lys Val Ser Arg Met Arg Cys Leu Gln Asn
500 505 510

Glu Thr Tyr Ser Ala Leu Ser Leu Ala Lys Val Arg Thr Leu Cys Phe
515 520 525

Arg Trp Ser Gln Glu Phe Ser Thr Leu Thr Leu Gly Gln Phe Gly
530 535 540

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGACCTTCCC AGCAATATGC ATCTTGCACG TCTGGTCCGC TCCTGCTCCC TCCTTCTGCT	60
ACTGGGGGCC CTGTCTGGAT GGGCGGCCAG CGATGACCCC ATTGAGAAGG TCATTGAAGG	120
GATCAACCGA GGGCTGAGCA ATGCAGAGAG AGAGGTGGGC AAGGCCCTGG ATGGCATCAA	180
CAGTGAATC ACGCATGCCG GAAGGGAAGT GGAGAAGGTT TTCAACGGAC TTAGCAACAT	240
GGGGAGCCAC ACCGGCAAGG AGTTGGACAA AGGCGTCCAG GGGCTCAACC ACGGCATGGA	300
CAAGGTTGCC CATGAGATCA ACCATGGTAT TGGACAAGCA GGAAAGGAAG CAGAGAAGCT	360
TGGCCATGGG GTCAACAACG CTGCTGGACA GGGCAACCAT CAAAGCGGAT CTTCCAGCCA	420
TCAAGGAGGG GCCACAACCA CGCCGTTAGC CTCTGGGGCC TCGGTCAACA CGCCTTTCAT	480
CAACCTTCCC GCCCTGTGGA GGAGCGTCGC CAACATCATG CCCTAAACTG GCATCCGGCC	540
TTGCTGGGAG AATAATGTCG CCGTTGTCAC ATCAGCTGAC ATGACCTGGA GGGGTTGGGG	600

GTGGGGGACA GGTTCCTGAA ATCCCTGAAG GGGGTTGTAC TGGGATTTGT GAATAAACTT 660
 GATACACTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
 AA 722

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	Leu	1	5	10	15
Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	Lys	Val	20	25	30	
Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	Glu	Val	Gly	35	40	45	
Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	Ala	Gly	Arg	Glu	50	55	60	
Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	Gly	Ser	His	Thr	Gly	65	70	75	80
Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	Asn	His	Gly	Met	Asp	Lys	85	90	95	
Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	Gly	Gln	Ala	Gly	Lys	Glu	Ala	100	105	110	
Glu	Lys	Leu	Gly	His	Gly	Val	Asn	Asn	Ala	Ala	Gly	Gln	Gly	Asn	His	115	120	125	
Gln	Ser	Gly	Ser	Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	130	135	140	
Ala	Ser	Gly	Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	145	150	155	160
Trp	Arg	Ser	Val	Ala	Asn	Ile	Met	Pro	165										

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1240 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATGGCTTTT CTTCCTTCCT GGGTTTGTGT ACTAGTTGGT TCCTTTTCTG CTTCCTTAGC	60
AGGGACTTCC AATCTCTCAG AGACAGAGCC CCCTCTGTGG AAGGAGAGTC CTGGTCAGCT	120
CAGTGACTAC AGGGTGGAGA ACAGCATGTA CATTATTAAT CCCTGGGTAT ACCTTGAGAG	180
AATGGGGATG TATAAAATCA TATTGAATCA GACAGCCAGG TATTTTGCAA AATTTGCACC	240
AGATAATGAA CAGAATATTT TATGGGGGTT GCCTCTGCAG TATGGCTGGC AATATAGGAC	300
AGGCAGATTA GCTGATCCAA CCCGAAGGAC AACTGTGGC TATGAATCTG GAGATCATAT	360
GTGCATCTCT GTGGACAGTT GGTGGGCTGA TTTGAATTAT TTTCTGTCTT CATTACCCTT	420
TCTTGCTGCG GTTGATTCTG GTGTAATGGG GATATCATCA GACCAAGTCA GGCTTTTGCC	480
CCCACCCAAG AATGAGAGGA AGTTTTGTGA TGATGTTTCT AGCTGTCGTT CATCCTTCCC	540
TGAGACAATG AACAAGTGGA ACACCTTTTA CCAGTATTTG CAGTCACCTT TTAGTAAGTT	600
TGATGATCTG TTGAAGTACT TATGGGCTGC ACACACTTCA ACCTTGGCAG ATAATATCAA	660
AAGTTTTGAA GACAGATATG ATTATTATTC TAAAGCAGAA GCGCATTTTG AGAGAAGTTG	720
GGTACTGGCT GTGGATCATT TAGCTGCAGT CCTCTTTCCT ACAACCTGA TTAGATCATA	780
TAAGTTCCAG AAGGGCATGC CACCACGAAT TCTTCTTAAT ACTGATGTAG CCCCTTTCAT	840
CAGTGACTTT ACTGCTTTTC AGAATGTAGT CCTGGTTCTT CTAAATATGC TTGACAATGT	900
GGATAAATCT ATAGGTTATC TTTGTACAGA AAAATCTAAT GTATATAGAG ATCATTCGGA	960
ATCTAGCTCT AGAAGTTATG GAAATAACTC CTGAAACATT TAACTTCAAA CTTCAGGAAA	1020
TGATTAATGA ATTAAAAATG AAAAAGCTGA ACTTGACAAT CAGTAATTTT AAAAAATTAA	1080
TGTCATCATG ACCATGTAGT TTATTCTTTC TGATATTTTT GATTATGCT TATTTGTTAA	1140
GATCTTGAC ATGTATTAAA AACTTAAATT AAATGCATTC AAGTTAAAAA AAAAAAAAAA	1200
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1240

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Ala	Phe	Leu	Pro	Ser	Trp	Val	Cys	Val	Leu	Val	Gly	Ser	Phe	Ser	1	5	10	15
Ala	Ser	Leu	Ala	Gly	Thr	Ser	Asn	Leu	Ser	Glu	Thr	Glu	Pro	Pro	Leu	20	25	30	
Trp	Lys	Glu	Ser	Pro	Gly	Gln	Leu	Ser	Asp	Tyr	Arg	Val	Glu	Asn	Ser	35	40	45	
Met	Tyr	Ile	Ile	Asn	Pro	Trp	Val	Tyr	Leu	Glu	Arg	Met	Gly	Met	Tyr	50	55	60	
Lys	Ile	Ile	Leu	Asn	Gln	Thr	Ala	Arg	Tyr	Phe	Ala	Lys	Phe	Ala	Pro	65	70	75	80
Asp	Asn	Glu	Gln	Asn	Ile	Leu	Trp	Gly	Leu	Pro	Leu	Gln	Tyr	Gly	Trp	85	90	95	
Gln	Tyr	Arg	Thr	Gly	Arg	Leu	Ala	Asp	Pro	Thr	Arg	Arg	Thr	Asn	Cys	100	105	110	
Gly	Tyr	Glu	Ser	Gly	Asp	His	Met	Cys	Ile	Ser	Val	Asp	Ser	Trp	Trp	115	120	125	
Ala	Asp	Leu	Asn	Tyr	Phe	Leu	Ser	Ser	Leu	Pro	Phe	Leu	Ala	Ala	Val	130	135	140	
Asp	Ser	Gly	Val	Met	Gly	Ile	Ser	Ser	Asp	Gln	Val	Arg	Leu	Leu	Pro	145	150	155	160
Pro	Pro	Lys	Asn	Glu	Arg	Lys	Phe	Cys	Tyr	Asp	Val	Ser	Ser	Cys	Arg	165	170	175	
Ser	Ser	Phe	Pro	Glu	Thr	Met	Asn	Lys	Trp	Asn	Thr	Phe	Tyr	Gln	Tyr	180	185	190	
Leu	Gln	Ser	Pro	Phe	Ser	Lys	Phe	Asp	Asp	Leu	Leu	Lys	Tyr	Leu	Trp	195	200	205	
Ala	Ala	His	Thr	Ser	Thr	Leu	Ala	Asp	Asn	Ile	Lys	Ser	Phe	Glu	Asp	210	215	220	
Arg	Tyr	Asp	Tyr	Tyr	Ser	Lys	Ala	Glu	Ala	His	Phe	Glu	Arg	Ser	Trp	225	230	235	240
Val	Leu	Ala	Val	Asp	His	Leu	Ala	Ala	Val	Leu	Phe	Pro	Thr	Thr	Leu	245	250	255	
Ile	Arg	Ser	Tyr	Lys	Phe	Gln	Lys	Gly	Met	Pro	Pro	Arg	Ile	Leu	Leu	260	265	270	
Asn	Thr	Asp	Val	Ala	Pro	Phe	Ile	Ser	Asp	Phe	Thr	Ala	Phe	Gln	Asn	275	280	285	

Val Val Leu Val Leu Leu Asn Met Leu Asp Asn Val Asp Lys Ser Ile
 290 295 300

Gly Tyr Leu Cys Thr Glu Lys Ser Asn Val Tyr Arg Asp His Ser Glu
 305 310 315 320

Ser Ser Ser Arg Ser Tyr Gly Asn Asn Ser
 325 330

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCAGCACCAG CCGTCTGCAG CTCCGGCCGC CACTTGCGCC TCTCCAGCCT CCGCAGGCCC	60
AACCGCCGCC AGCACCATGG CCAGCACCAT TTCCGCCTAC AAGGAGAAGA TGAAGGAGCT	120
GTCGGTGCTG TCGCTCATCT GCTCCTGCTT CTACACACAG CCGCACCCCA ATACCGTCTA	180
CCAGTACGGG GACATGGAGG TGAAGCAGCT GGACAAGCGG GCCTCAGGCC AGAGCTTCGA	240
GGTCATCCTC AAGTCCCCTT CTGACCTGTC CCCAGAGAGC CCTATGCTCT CCTCCCCACC	300
CAAGAAGAAG GACACCTCCC TGGAGGAGCT GCAAAAGCGG CTGGAGGCAG CCGAGGAGCG	360
GAGGAAGACG CAGGAGGCGC AGGTGCTGAA GCAGCTGGCG GAGCGGCGCG AGCACGAGCG	420
CGAGGTGCTG CACAAGGCGC TGGAGGAGAA TAACAACTTC AGCCGCCAGG CGGAGGAGAA	480
GCTCAACTAC AAGATGGAGC TCAGCAAGGA GATCCGCGAG GCACACCTGG CCGCACTGCG	540
CGAGCGGCTG CGCGAGAAGG AGCTGCACGC GGCCGAGGTG CGCAGGAACA AGGAGCAGCG	600
AGAAGAGATG TCGGGCTAAG GGCCCGGGAC GGGCGGCGCC CATCCTGCGA CAGAACACGT	660
TCGGGTTTTG GTTTTGTTC GTTCACCTCT GTCTAGATGC AACTTTTGTT CCTCCTCCCC	720
CACCCAGCC CCCAGCTTCA TGCTTCTCTT CCGCACTCAG CCGCCCTGCC CTGTCTCTGT	780
GGTGAGTCGC TGACCACGGC TTCCCCTGCA GGAGCCGCCG GGCCTGAGAC GCGGTCCCTC	840
GGTGCAGACA CCAGGCCGGG CGCGGCTGGG TCCCCGGGG GCCCTGTGAG AGAGGTGGCG	900
GTGACCGTGG TAAACCCAGG GCGGTGGCGT GGGATCGCGG GTCCTTACGC TGGGCTGTCT	960
GGTCAGCACG TGCAGGTCAG GGCAGGTCCT CTGAGCCGGC GCCCTGGCC AGCAGGCGAG	1020
GCTACAGTAC CTGCTGTCTT TCCAGGGGGA AGGGGCTCCC CATGAGGGAG GGGCGACGGG	1080

GGAGGGGGGT GATGGTGCCT GGGAGCCTGC GTGTGCAGCC GGTGCTTGTT GAACTGGCAG 1140
GCGGGTGGGT GGGGGCTGCA GCTTTCCTTA ATGTGGTTGC ACAGGGGTCC TCTGAGACCA 1200
CCTGGCGTGA GGTGGACACC CTGGGCCTTC CTGGAAGCCT GCAGTTGGGG GCCTGCCCTG 1260
AGTCTGCTGG GGAGTGGGCA TTCTCTGCCA GGGACCCATG AGCAGGCTGC ATGGTCTAGA 1320
GGTTGTGGGC AGCATGGACA GTCCCCCACT CAGAAGTGCA AGAGTTCCAA AGAGCCTCTG 1380
GCCCAGGCCC CTCCCCACCA GGGCTTTGCA GATGTCCTTG AAAGACCCAC CCTAGAGCCC 1440
TTTGGAGTGC TGGCCCCCTCC TGTGCCCTCT GCCCTGGTGG AAGCGGCAGC CACAAGTCCT 1500
CCTCAGGGAG CCCC AAGGGG GATTTTGTGG GACCGCTGCC CACAGATCCA GGTGTTGGAA 1560
GGGCAGCGGG TAAGGTTCCT AAGCCAGCCC CAACACCCTT CCCACTTGGC ACCCAGAGGG 1620
GGCTGTGGGT GGAGGCCTGA CTCCAGGCCT CTCCTGCCCA CACCCTCTGG GCTGAGTTCC 1680
TTCTTTCCT TGGACGCCCA GTGCTGGCCT TGGAGGACGG TCAGCTGGAG GATGGCGGTG 1740
GGGGAGGCTG TCTTTGTACC ACTGCAGCAT CCCCCACTTC TCCACGGAAG CCCCATCCCA 1800
AAGCTGCTGC CTGGCCCCCTT GCTGTAAAGT GTGAAGGGGG CGGCTGAGTT CTCTTAGGAC 1860
CCAGAGCCAG GGCCCTCAAC TTCCATCCTG CGGGAGGCCT TGGCCGGGCA CTGCCAGTGT 1920
CTTCCAGAGC CACACCCAGG GACCACGGGA GGATCCTGAC CCCTGCAGGG CTCAGGGGTC 1980
AGCAGGGACC CACTGCCCCA TCTCCCTCTC CCCACCAAGA CAGCCCCAGA AGGAGCAGCC 2040
AGCTGGGATG GGAACCCAAG GCTGTCCACA TCTGGCTTTT GTGGGACTCA GAAAGGGAAG 2100
CAGAACTGAG GGCTGGGATA TTCCTCATGG TGGCAGCGCT CATAGCGAAA GCCTACTGTA 2160
ATATGCACCC ATCTCATCCA CGTAGTAAAG TGAACTTAAA AATCAATCA AATGAACAAT 2220
TAAATAAACA CCTGTGTGTT TAAGAAAAAA AAAAAAAAAA A 2261

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ala Ser Thr Ile Ser Ala Tyr Lys Glu Lys Met Lys Glu Leu Ser
1 5 10 15

Val Leu Ser Leu Ile Cys Ser Cys Phe Tyr Thr Gln Pro His Pro Asn
20 25 30

Thr	Val	Tyr	Gln	Tyr	Gly	Asp	Met	Glu	Val	Lys	Gln	Leu	Asp	Lys	Arg	
			35				40					45				
Ala	Ser	Gly	Gln	Ser	Phe	Glu	Val	Ile	Leu	Lys	Ser	Pro	Ser	Asp	Leu	
		50				55					60					
Ser	Pro	Glu	Ser	Pro	Met	Leu	Ser	Ser	Pro	Pro	Lys	Lys	Lys	Asp	Thr	
		65			70					75					80	
Ser	Leu	Glu	Glu	Leu	Gln	Lys	Arg	Leu	Glu	Ala	Ala	Glu	Glu	Arg	Arg	
				85					90					95		
Lys	Thr	Gln	Glu	Ala	Gln	Val	Leu	Lys	Gln	Leu	Ala	Glu	Arg	Arg	Glu	
			100					105					110			
His	Glu	Arg	Glu	Val	Leu	His	Lys	Ala	Leu	Glu	Glu	Asn	Asn	Asn	Phe	
			115				120					125				
Ser	Arg	Gln	Ala	Glu	Glu	Lys	Leu	Asn	Tyr	Lys	Met	Glu	Leu	Ser	Lys	
		130				135					140					
Glu	Ile	Arg	Glu	Ala	His	Leu	Ala	Ala	Leu	Arg	Glu	Arg	Leu	Arg	Glu	
		145			150				155						160	
Lys	Glu	Leu	His	Ala	Ala	Glu	Val	Arg	Arg	Asn	Lys	Glu	Gln	Arg	Glu	
				165				170						175		
Glu	Met	Ser	Gly													
			180													

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCCAAAGAG GCCTAGGAGC CTCGTGGCTG CGTCACCGCC GCCCCCCCAG ACAAGATGGA	60
CACCGCGGAG GAAGACATAT GTAGAGTGTG TCGGTCAGAA GGAACACCTG AGAAACCGCT	120
TTATCATCCT TGTGTATGTA CTGGCAGTAT TAAGTTTATC CATCAAGAAT GCTTAGTTCA	180
ATGGCTGAAA CACAGTCGAA AAGAATACTG TGAATTATGC AAGCACAGAT TTGCTTTTAC	240
ACCAATTTAT TCTCCAGATA TGCCTTCACG GCTTCCAATT CAAGACATAT TTGCTGGACT	300
GGTTACAAGT ATTGGCACTG CAATACGATA TTGGTTTCAT TATACACTTG TGGCCTTTGC	360
ATGGTTGGGA GTTGTTCCTC TTACAGCATG CCGCATCTAC AAGTGCTTGT TTAGTGGCTC	420
CCGTGAGCTC ACTACTGACG CTGCCCATTA GATATGCTGT CAACCGGAAA ATTTGTTGGC	480

AGATTGTTTG	CAGGGTTGTT	TTGTGGTGAC	GTGCACACTG	TGTGCATTCA	TCAGCCTGGT	540
GTGGTTGAGA	GAGCAGATAG	TCCATGGGGG	AGCACCAATT	TGGTTGGAGC	ATGCTGCCCC	600
ACCGTTCAAT	GCTGCGGGGC	ATCACCAAAA	TGAGGCTCCA	GCAGGAGGAA	ATGGTGCAGA	660
AAATGTTGCT	GCTGATCAGC	CTGCTAACCC	ACCAGCTGAG	AACGCAGTGG	TGGGGGAAAA	720
CCCTGATGCC	CAGGATGACC	AGGCAGAAGA	GGAGGAGGAG	GACAATGAGG	AGGAAGATGA	780
CGCTGGTGTG	GAGGATGGCG	GCAGATGCTA	ATAACGGAGC	CCAGGATGAC	ATGAATTGGA	840
ATGCTTTAGA	ATGGGACCGA	GCTGCTGAAG	AGCTTACATG	GGAAAGAATG	CTAGGACTTG	900
ATGGATCACT	AGTTTTTCTG	GAACATGTCT	TCTGGGTGGT	ATCTTTAAAT	ACACTGTTCA	960
TTCTTGTTTT	TGCATTTTGC	CCTTACCATA	TTGGTCATTT	CTCCCTTGTT	GGTTTGGGAT	1020
TTGAAGAACA	CGTCCAAGCA	TCTCATTTTG	AAGGCCTAAT	CACAACCATA	GTTGGGTATA	1080
TACTTTTAGC	AATAACACTG	ATAATTTGTC	ATGGCTTGGC	AACTCTTGTTG	AAATTTTCATA	1140
GATCTCGTCG	CTTACTGGGA	GTCTGCTATA	TTGTTGTTAA	GGTCTCTTTG	TTAGTGGTGG	1200
TAGAAATTGG	AGTATTCCCT	CTCATTTGTG	GTTGGTGGCT	GGATATCTGT	TCCTTGGAAG	1260
TGTTTGATGC	TACTCTGAAA	GATCGAGAAC	TGAGCTTTCA	GTCGGCTCCA	GGTACTACCA	1320
TGTTTCTGCA	TTGGCTAGTG	GGAATGGTAT	ATGTCTTCTA	CTTTGCCTCC	TTCATTCTAT	1380
TACTGAGAGA	GGTACTTCGA	CCTGGTGTCC	TGTGGTTTCT	AAGGAATTTG	AATGATCCAG	1440
ATTTCAATCC	AGTACAGGAA	ATGATCCATT	TGCCAATATA	TAGGCATCTC	CGAAGATTTA	1500
TTTTGTCACT	GATTGTCTTT	GGCTCCATTG	TCCTCCTGAT	GCTTTGGCTT	CCTATACGTA	1560
TAATTAAGAG	TGTGCTGCCT	AATTTTCTTC	CATACAATGT	CATGCTCTAC	AGTGATGCTC	1620
CAGTGAGTGA	ACTGTCCCTC	GAGCTGCTTC	TGCTTCAGGT	TGTCTTGCCA	GCATTACTCG	1680
AACAGGGACA	CACGAGGCAG	TGGCTGAAGG	GGCTGGTGCG	AGCGTGGACT	GTGACCGCCG	1740
GATACTTGCT	GGATCTTCAT	TCTTATTTAT	TGGGAGACCA	GGAAGAAAAT	GAAAACAGTG	1800
CAAATCAACA	AGTTAACAAT	AATCAGCATG	CTCGAAATAA	CAACGCTATT	CCTGTGGTGG	1860
GAGAAGGCCT	TCATGCAGCC	CACCAAGCCA	TACTCCAGCA	GGGAGGGCCT	GTTGGCTTTT	1920
AGCCTTACCG	CCGACCTTTA	AATTTTCCAC	TCAGGATATT	TCTGTTGATT	GTCTTCATGT	1980
GTATAACATT	ACTGATTGCC	AGCCTCATCT	GCCTTACTTT	ACCAGTATTT	GCTGGCCGTT	2040
GGTTAATGTC	GTTTTGGACG	GGGACTGCCA	AAATCCATGA	GCTCTACACA	GCTGCTTGTC	2100
GTCTCTATGT	TTGCTGGCTA	ACCATAAGGG	CTGTGACGGT	GATGGTGGCA	TGGATGCCTC	2160
AGGGACGCAG	AGTGATCTTC	CAGAAGGTTA	AAGAGTGGTC	TCTCATGATC	ATGAAGACTT	2220

TGATAGTTGC GGTGCTGTTG GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC 2280
 TGGTCATTGT GGCTCCCCTG AGGGTTCCCT TGGATCAGAC TCCTCTTTTT TATCCATGGC 2340
 AGGACTGGGC ACTTGGAGTC CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC 2400
 CTCAGTGGTG GTTGAAAACCT GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG 2460
 ACCTTCACTA TATTGTTTCGT AAACCTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC 2520
 TGTGTGTACC TTATGTCATA GCTTCTGGTG TTGTTCTTTT ACTAGGTGTT ACTGCGGAAA 2580
 TGCAAAACTT AGTCCATCGG CGGATTTATC CATTTTTACT GATGGTCGTG GTATTGATGG 2640
 CAATTTTGTC CTTCCAAGTC CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA 2700
 AGTACCTTGK GGGTCAASGA CTCGGTGAAC TACGAACGGA AATCTGGGCA AACAAGGCTC 2760
 ATCTCCACCA CCTCCACAGT CATCCCAAGA ATAAAGTAGT TGTCTCAACA ACTTGACCTT 2820
 CCCCTTTACA TGTCCTTTTT TGTGGACTTC TCTCTTKGGA GATTTTTCCC AGTGATCTCT 2880
 CAGCGTKGTT TTTAAGTTAA AKGTATTKGA CTTGTGTTCT CAGCATTCAG AGAGCAGCGG 2940
 TGTAAGATTC TGCTGTTCTC CCTGGATCTT CTGACATKAC TGCTGTCTGA GATTTGTATA 3000
 TGKGTAAATA CAAGTTCCTT GATACCCTAA AACCTTGGAT TAAACAGAAT GTGCATKGTA 3060
 CATCTTTAAA CAAAATGKAT ATTAATTTAT TAAAAAAAAA AAAAAAAAAA 3109

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Gly	Glu	His	Gln	Phe	Gly	Trp	Ser	Met	Leu	Pro	His	Arg	Ser	Met
1				5					10					15	
Leu	Arg	Gly	Ile	Thr	Lys	Met	Arg	Leu	Gln	Gln	Glu	Glu	Met	Val	Gln
			20					25					30		
Lys	Met	Leu	Leu	Leu	Ile	Ser	Leu	Leu	Thr	His	Gln	Leu	Arg	Thr	Gln
		35					40					45			
Trp	Trp	Gly	Lys	Thr	Leu	Met	Pro	Arg	Met	Thr	Arg	Gln	Lys	Arg	Arg
	50					55					60				
Arg	Arg	Thr	Met	Arg	Arg	Lys	Met	Thr	Leu	Val	Trp	Arg	Met	Ala	Ala
65					70					75				80	

Val	Val	Leu	Met	Ala	Ile	Leu	Ser	Phe	Gln	Val	Arg	Gln	Phe	Lys	Arg
690						695					700				
Leu	Tyr	Glu	His	Ile	Lys	Asn	Asp	Lys	Tyr	Leu	Xaa	Gly	Gln	Xaa	Leu
705					710					715					720
Gly	Glu	Leu	Arg	Thr	Glu	Ile	Trp	Ala	Asn	Lys	Ala	His	Leu	His	His
				725					730					735	
Leu	His	Ser	His	Pro	Lys	Asn	Lys	Val	Val	Val	Ser	Thr	Thr		
				740				745					750		

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TNTTTGAAGT TTCTCCCTCT CATTCTGAG

29

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GNTTCTCCAC GTAGTTGGTT TTCCTCAGT

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CNACATGACG TGAGCTGGTG ATCCATGAA

29

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ANTTGGGCTC TGCCGTCCAG AAAGGTTTG

29

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GNAGCTACGC GGACTTGCAG AGGTTTTAT

29

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNGGTGAGAG AATAGAGACT GGCTGGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANGAGCCGAC CAGACGTGCA AGATGCATA

29

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ANCTGACCAG GACTCTCCTT CCACAGAGG

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TNTAGGCGGA AATGGTGCTG GCCATGGTG

29

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
ANATATCCAG CCACCAACCA CAAATGAGA

29

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCTAATTTGA GAAGAAAACA AGTAGGATTT TTGTTTTGTT TTGCATTTTG CAATATGGAG	60
GAGAAATGAT TAGACCTTAG GAAGTGCCAG TGGGTTGGTC CTTTCATGAA CATGCCATCA	120
GTAAAAGCCC TGGAAACAAG GTCATACCAG AGATTCATTG TGCCTTGTC CAACTGCAAA	180
CAATATCTGA GTGGAATATT CAAAACTTG CTTAGAAAGA AAACCTTAGG ACAGATGGCT	240
CCACTGAAGT TATTCCAAAT ATTTAATAAA TAAAGCATAC CAGGCTTTTA TAACTCTTC	300
TAGAAGAAAA AAGTTGGAAC TTTTCCAATT CAGTTTTTCA GGCCAGTGCA ACCTTGATAC	360
CAAAACCAAT AAAACAAACA AACAAACAAA AAACATAAAG CTATAGACCA AAGTCTCATA	420
GATTTAGATG CAAAATCCTA AAATTGAAAA AAAAAGTCTA GTCATATCCA TAACTGTAT	480
CATCACCAAG AGATGTTTAT TAGGGCAATC AAAAGATGAT TTATTATTTT TAAAAAATC	540
AATGTGGCCT TCCCTTCCTC TTTCTTTTGA TTCCCTCTT TGAGTTTTTA TGTGTCTCTT	600
TTGCCTTCCC TTCCCAGAGT GGAGGAGTTA GACCTGCATT GTGGGATGAG AGGAGTTGTG	660
GCTATGTGTC TGCTGGCACC AAGAGGGCTG AGGGTGAGGT GTGGAAGGGA CAGGGGGAGG	720
AGATGGGCAG CATTGTTAAG AGATTGGTAC CACTGAGCAA ATATGTTGAG AATGATGATG	780

GCAAGGTTTC TCCCTGTTAG AGAAGGTATT TGTAGAAATA GGAATGAGGA GAGCTAGAAA 840
 ACCTGGAGTG TGGGATTAGA ATAGAACTCA TATCTTTTAA ATACATAGGA ACAATAGAGA 900
 AATTGTTGGG TGTGCCCATA TACATATATT TTGTGATTCA TTCTACCGAG AGGACATAAA 960
 TGCAGTCACA GCTCAGTAAC AGTAAACACA CCAACTGCCA AGTTATTATT TCCTAAATAC 1020
 TATCCACAAA AAAGGGGACC AGGGATGATT CCTAGTCGGA GATTGGGAGA AAAAGAAGAT 1080
 GAGCCTGAAT CATTTTCATGT ACCTAACAGA AAGAAAATAC TCTGGCTGGG CTCAGWGGCT 1140
 CATGTTTGTA ATTCTAGCAT GTTAGGAGGT CGAGGTGGGT GTGTTGCTTG AGCCCAGGAG 1200
 TTTGAGACCA GCCCAGGCAA CATGGCAAAA CTGTCTCTAC AAAAAATATA AAAGTTAGCC 1260
 AGGCGTGGTG GCATGCGCCT GTCGTCCGAG ATACTCGGGA GGCAGAGAGG TGGGAGGATC 1320
 ACTTGAGCCT GGGAGATTGA GACTGCATCG AGCTGTGGTC ATGCCACTGC ACTCCAGCCT 1380
 GGAGGACAGA GTGAGACCCT GTCTCAGGAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met	Ile	Tyr	Tyr	Phe	Leu	Lys	Asn	Gln	Cys	Gly	Leu	Pro	Phe	Leu	Phe	1	5	10	15
Leu	Leu	Ile	Pro	Leu	Phe	Glu	Phe	Leu	Cys	Val	Ser	Phe	Ala	Phe	Pro	20	25	30	
Ser	Gln	Ser	Gly	Gly	Val	Arg	Pro	Ala	Leu	Trp	Asp	Glu	Arg	Ser	Cys	35	40	45	
Gly	Tyr	Val	Ser	Ala	Gly	Thr	Lys	Arg	Ala	Glu	Gly	Glu	Val	Trp	Lys	50	55	60	
Gly	Gln	Gly	Glu	Glu	Met	Gly	Ser	Ile	Val	Lys	Arg	Leu	Val	Pro	Leu	65	70	75	80
Ser	Lys	Tyr	Val	Glu	Asn	Asp	Asp	Gly	Lys	Val	Ser	Pro	Cys			85	90		

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2859 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCACCCAGC	CGCGCCGGCG	AGGACATGGG	CAGCCGCGGC	GCGCCCACCC	CCC	CGCCGA	60
TGTGAATTAT	TAAAAAGAAA	ATGGCCCAAC	GGAGCACTGT	ATTCCTTCT	CGT	GTACCA	120
AGGAAAGGTA	TAATATATGG	AAAATATGCA	TCTAAGGCGA	GTGAGAACCA	TGCCCC	GACA	180
CAGCCAGTCC	CTGACCATGG	CACCATACTC	ATCTGTAAGC	CTCGTGAGC	AGCTGGAAGA		240
CAGGATCCTC	TGCCATGAGA	AAACCACCGC	CGCCCTCGTA	GAGCACGCCT	TTCGGATTAA		300
AGATGACATT	GTCAACAGTT	TGCAGAAAAT	GCAAAACAAA	GGGGGAGGTG	ACCGCTTGGC		360
CAGGCTTTTC	TTGGAGGAGC	ATATCAGAAA	CATAACTGCC	ATAGTGAAGC	AACTTAATCG		420
GGATATCGAG	GTACTCCAGG	AGCAGATTCT	TGCTCGGGAC	AACATTAGCT	ATGGAATAA		480
TTCTGCCTTA	AAGACCCTGG	AGATGCGCCA	GCTCTCCGGT	TTGGGAGATC	TTCGAGGAAG		540
AGTGGCAAGA	TGTGATGCCA	GCATAGCTAG	ACTTTCTGCA	GAGCACAAAA	CGACCTATGA		600
GGGGCTCCAG	CACTTGAACA	AAGAACAGCA	GGCTGCCAAA	CTTATCTTGG	AAACGAAAAT		660
CAAAGATGCA	GAGGGACAGA	TTTCTCAGCT	TTTGAACAGA	GTGGACTTGT	CAATATCAGA		720
GCAGAGCACC	AAACTGAAGA	TGTCTCACAG	AGACAGTAAC	CACCAGCTTC	AGCTTTTGGA		780
CACTAAATTT	AAAGGTACAG	TTGAGGAACT	CAGTAACCAG	ATATTATCTG	CACGGAGTTG		840
GTTGCAACAG	GAACAAGAAC	GGATAGAAAA	AGAGCTTTTA	CAGAAAATTG	ATCAGCTTTC		900
CTTGATTGTT	AAGGAAAACA	GTGGAGCCAG	TGAAAGGGAT	ATGGAGAAGA	AGCTCAGCCA		960
GATGTCAGCC	AGGCTTGACA	AAATAGAAGA	GGGTCAAAAG	AAGACTTTTG	ATGGTCAGAG		1020
AACAAGGCAA	GAAGAGGAGA	AGATGCACGG	GCGAATCACC	AAGCTGGAGT	TACAGATGAA		1080
CCAGAACATC	AAGGAAATGA	AAGCAGAAGT	TAATGCTGGG	TTTACAGCCG	TCTATGAAAG		1140
CATAGGATCC	CTCAGGCAAG	TTCTCGAGGC	CAAGATGAAG	CTGGACAGGG	ACCAGCTACA		1200
GAAGCAAATC	CAGCTGATGC	AGAAGCCAGA	GACCCCCATG	TGAAGGGAGC	TGGGACAAGG		1260
TCCTAAAAGA	CAGTTTTGCC	AGTGGGGCTA	GGAGCCGGAT	ACCTCTGTAG	CCAGGCCATC		1320
GCTGCATTCA	GGATTGTTCC	ATCCATGGCG	TGCATGTGCC	AAGAAATGTG	TTTTTATGGG		1380
TCTAAATGTT	TACCTTGAGT	CTTGAAAATA	CTCTTTTGTT	AAAAGTATGA	AATACAGTTT		1440

TTACCAGTTT	ATTTCACTTC	TCTAAATTCA	ATGGAAATCC	CCCGCCCTGG	ATTTTGAAAG	1500
GCTTTTATCT	TCTTCATTTT	ACGAATGGAA	AGACGACAAT	TTTTCTTCAA	TGCTTGATGC	1560
ACTAATGAAG	ACTGTTTACT	ATTTTGAAAA	ATGTCATGGG	GATTTTTTTT	TAATTAAGAA	1620
ACTAATGAAT	CATCACAGGA	ATGTGTTGCT	CCTCACCTTA	AATTAAGAGA	ATGTCCCAGT	1680
AGATTAGACT	TCAACCTTTG	AGTCCAATTT	GGATTTTATT	ATCGTTGTCT	ATGCACTTCT	1740
TATATTGGTT	ATCTTCTTGT	AAATCTTCTG	TCTTTTGTA	GGGGAAAGGA	TTTAACATTT	1800
AGAATAAACC	CCACCATTTA	TGTAATGGAA	ATAGTTTAAA	AATTGCTAAC	TGCCATGTGG	1860
ATTGCAAATT	AAATGGAAAC	TTATTTAGAT	AACGTAAGGC	TCAATATCTG	CGTTGACCAC	1920
CTAGATATTA	CAGGTTTTAA	TATTTAAAAC	TATTTTTGAA	TTATCCACAA	CCTGTATAGT	1980
GATAGCCATA	TATTTAATAA	TGGAATGGTG	GTAAACAGTC	TATTTACTGC	ACAATTAATT	2040
GTTCACTAAT	CAAATAGAAT	GTGGTAATTT	TTCAGACTTT	ATGATCTGTT	TCCAAAATTG	2100
GCACAAAGTG	CTAGGGTTTA	TATACACTTA	TCGTAAGTGT	ATTTTTGTGC	CTTGGTTTTA	2160
TCATGTCAAT	GCACTGTACT	CTGTAAAAGT	TTTGACAGAC	AAATAGAAAG	TATGATAATC	2220
CGTCAGAAGT	ATGATGTAAA	ACTGGAATCC	TCTGTATTTT	TTAAATGTTC	TAAAAATTTT	2280
ATCGCTGTTA	AGGTATTAAT	CATTCACTAT	TACTAATGGA	ATAGAAATTC	ATACTTTTGT	2340
ATGGACAACA	AATTGATATT	GCATTTATAG	CACTGTAAGA	AACTTTCATC	TTGAGCAACT	2400
TTGTAGATGA	TGGGTGTTTT	ATTTTCAATC	GCCATATTTG	ATCAGTCATT	GAAAATTGGC	2460
CCCAGTGCTG	TTTGTTTCATC	TCTGTATGTA	AAAAGTACAC	GTGAGACACA	ACTTTCTGAA	2520
CTGTGAGGGT	GTCCCAGGAA	AAAGAAAAAC	AGGAATACTT	TAACAATTAA	AAAGAAAAAA	2580
ATGTTTTTTT	TTTGCCAAGG	ACTCAGGAAA	ATAAAAAGCA	TTTTCTATTT	TTAGGACAAA	2640
TCACAAATGA	AGTGTCTAAC	TGGCTATTAC	TGTTTACCCA	TATAAAATAT	GCTGCTAAAG	2700
TACATATTTT	GCTGTCAATG	GCTTGACAAT	TTTTTTTTTC	AAATTGGAC	ATGAGAGGTT	2760
ATATAGGGAC	TATATTATCC	AACACATATT	TTCTTATTTT	GCCACAAATT	TCCACTTAAC	2820
AAATAAAAAA	AGGCGAATGC	TGTTTTGCAA	AAAAAAAAAA			2859

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Glu	Asn	Met	His	Leu	Arg	Arg	Val	Arg	Thr	Met	Pro	Arg	His	Ser	1	5	10	15
Gln	Ser	Leu	Thr	Met	Ala	Pro	Tyr	Ser	Ser	Val	Ser	Leu	Val	Glu	Gln	20	25	30	
Leu	Glu	Asp	Arg	Ile	Leu	Cys	His	Glu	Lys	Thr	Thr	Ala	Ala	Leu	Val	35	40	45	
Glu	His	Ala	Phe	Arg	Ile	Lys	Asp	Asp	Ile	Val	Asn	Ser	Leu	Gln	Lys	50	55	60	
Met	Gln	Asn	Lys	Gly	Gly	Gly	Asp	Arg	Leu	Ala	Arg	Leu	Phe	Leu	Glu	65	70	75	80
Glu	His	Ile	Arg	Asn	Ile	Thr	Ala	Ile	Val	Lys	Gln	Leu	Asn	Arg	Asp	85	90	95	
Ile	Glu	Val	Leu	Gln	Glu	Gln	Ile	Arg	Ala	Arg	Asp	Asn	Ile	Ser	Tyr	100	105	110	
Gly	Thr	Asn	Ser	Ala	Leu	Lys	Thr	Leu	Glu	Met	Arg	Gln	Leu	Ser	Gly	115	120	125	
Leu	Gly	Asp	Leu	Arg	Gly	Arg	Val	Ala	Arg	Cys	Asp	Ala	Ser	Ile	Ala	130	135	140	
Arg	Leu	Ser	Ala	Glu	His	Lys	Thr	Thr	Tyr	Glu	Gly	Leu	Gln	His	Leu	145	150	155	160
Asn	Lys	Glu	Gln	Gln	Ala	Ala	Lys	Leu	Ile	Leu	Glu	Thr	Lys	Ile	Lys	165	170	175	
Asp	Ala	Glu	Gly	Gln	Ile	Ser	Gln	Leu	Leu	Asn	Arg	Val	Asp	Leu	Ser	180	185	190	
Ile	Ser	Glu	Gln	Ser	Thr	Lys	Leu	Lys	Met	Ser	His	Arg	Asp	Ser	Asn	195	200	205	
His	Gln	Leu	Gln	Leu	Leu	Asp	Thr	Lys	Phe	Lys	Gly	Thr	Val	Glu	Glu	210	215	220	
Leu	Ser	Asn	Gln	Ile	Leu	Ser	Ala	Arg	Ser	Trp	Leu	Gln	Gln	Glu	Gln	225	230	235	240
Glu	Arg	Ile	Glu	Lys	Glu	Leu	Leu	Gln	Lys	Ile	Asp	Gln	Leu	Ser	Leu	245	250	255	
Ile	Val	Lys	Glu	Asn	Ser	Gly	Ala	Ser	Glu	Arg	Asp	Met	Glu	Lys	Lys	260	265	270	

Leu Ser Gln Met Ser Ala Arg Leu Asp Lys Ile Glu Glu Gly Gln Lys
 275 280 285
 Lys Thr Phe Asp Gly Gln Arg Thr Arg Gln Glu Glu Glu Lys Met His
 290 295 300
 Gly Arg Ile Thr Lys Leu Glu Leu Gln Met Asn Gln Asn Ile Lys Glu
 305 310 315 320
 Met Lys Ala Glu Val Asn Ala Gly Phe Thr Ala Val Tyr Glu Ser Ile
 325 330 335
 Gly Ser Leu Arg Gln Val Leu Glu Ala Lys Met Lys Leu Asp Arg Asp
 340 345 350
 Gln Leu Gln Lys Gln Ile Gln Leu Met Gln Lys Pro Glu Thr Pro Met
 355 360 365

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGCTTCGGAG ACCGTAAGGA TATTGATGAC CATGAGATCC CTGCTCAGAA CCCCTTCCT	60
GTGTGGCCTG CTCTGGGCCT TTTGTGCCCC AGGCGCCAGG GCTGAGGAGC CTGCAGCCAG	120
CTTCTCCCAA CCCGGCAGCA TGGGCCTGGA TAAGAACACA GTGCACGACC AAGAGTACGT	180
ATTCAGCCCG GGCTGTGGTC CAGTGGCCTC CCCATCATCT GCAGCTGAGC CAGCGGCAAG	240
GGCATGCTCA GTCCTCCTTT CTTTCTTCCT GTTTCTATGG CTCCTTGACA TTCTTCAAGG	300
ATGATTCTTA TTCCTTATTG CCACCTATAA GTCAGGTATT CTTTTTTCAT CATTGTATCA	360
CAGGTGGAAG ATCTTTAGGC CCAAATGGGG CACATTACTT GTCTGAATCC GGTCTCTCCT	420
TTTTTTCACC ACAGACAGAC ACACACACAT ACAAATAGAC ACACAGGTAC ACATACACAG	480
TCATAGTAGC AGAATCCAGA AAATAGCTAA GGTTCCTTGA CTATAACAAG ACCTTTTTTTA	540
AATCAACACA TTCAAACATT GAATCATTTG TTGCAGCTTT TGTCTTGGGC CAGTTAGCCT	600
CACGCATTAT ACTCGGTTAT CCTTTGTTTT TAAGGCTGGG TGCAGTGGCT CACACCTGTA	660
ATCCAGTGC TTTGGGAGGC TGAGGCAGGT GGATTACTTG AGCCCAGGAA TTCGAGACCA	720

GCCTAGGCAA TATAGGGAAA ACCTGTCTCT AYTAAAAAAT TGCAAAAAAT TAGCTGGATG 780
 TGGCAGTACA TGCCTATGGT CCCAGCTACT TGGGGGGCTG AAGTGGGAGA ATCAAMTGAG 840
 CTTGGGAAGT TGAGGCTACA ATGAGCCAAG ATCAGCTCC TGCACTCCAG CCTGGGTGGC 900
 AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA AAA 933

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Thr	Met	Arg	Ser	Leu	Leu	Arg	Thr	Pro	Phe	Leu	Cys	Gly	Leu	Leu
1				5					10					15	
Trp	Ala	Phe	Cys	Ala	Pro	Gly	Ala	Arg	Ala	Glu	Glu	Pro	Ala	Ala	Ser
			20					25					30		
Phe	Ser	Gln	Pro	Gly	Ser	Met	Gly	Leu	Asp	Lys	Asn	Thr	Val	His	Asp
			35				40					45			
Gln	Glu	Tyr	Val	Phe	Ser	Pro	Gly	Cys	Gly	Pro	Val	Ala	Ser	Pro	Ser
	50						55				60				
Ser	Ala	Ala	Glu	Pro	Ala	Ala	Arg	Ala	Cys	Ser	Val	Leu	Leu	Ser	Phe
65						70				75				80	
Phe	Leu	Phe	Leu	Trp	Leu	Leu	Asp	Ile	Leu	Gln	Gly				
				85					90						

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2956 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

05745783.123400

GGTGTGTGGT	GGTTTAAGAA	TGTATATCAT	AGGGTCAGGT	GGCCTGGGTT	CATTCCCCAG	60
CTACGTAACC	TTTCTATGCC	TGAGTTTCCT	CATCTATAAA	ACAAGGATAA	TAATAGTGTG	120
TACTTCTTAG	GATTGTTTTG	GAGACTCATA	AATGAGAAAT	ACGTGAAAAA	CTCCCTCAAG	180
GCAGTGCTTG	ACACATAATG	AGCACTCAGT	TATCATGGTC	ATCATGGTCA	TCATCACTGC	240
TACCACCACT	GCTGCTGCTA	TTACCACTCT	ACCTCTTCCC	CCTGAAACTC	TAATCACTTA	300
CCCTAGAAAC	AGTTAAATTA	CACTTCAGTG	GGAAGGATCT	CAGATTTCTT	AATGGCACCT	360
GCATTTATAT	AATGTTGATA	TTGCACGTTT	CTAGAAAACA	TATCAAGAAG	AAACCAAAT	420
GTGTTTCTGT	ACTTTGTAAA	CCTGTACAAT	AGTTAGAGAT	TAGAGGACCT	TTATAATCTA	480
CTACTAATTA	CTGTGAAAGT	AAACATTGTT	TAATATACCA	GTTCTTAAAG	AAATATTTTG	540
TCTAGTCATT	AATATTCTAG	TTCATCTCAA	AGCTTCCATT	TGACAATTTA	AAATTACTTA	600
AATTTTAATA	TTAAAGGAAA	CAGTTTTCTT	GATTCTCATG	AAAGTTCCTA	TTTGCCTGA	660
AGATGACTAA	ACCTTTTAGT	CATAGTTTTA	GAAGAATTGG	CTTTTTTATA	GCCATTTTAT	720
TTACATATGG	GTAATGCATA	GCAAAGGCAG	CAGATTAGCC	CTGTTTGTTT	TGCAGGGATG	780
AAAGGTAGCA	TTCCCAGAGA	TTAAGTTGTT	CTTGCTATTC	CCATTCTCTG	CTACATTTGC	840
CTACATTCTT	TGGTCCTTTC	TATTATTTGT	TTCTTTGGTG	GAATCCCCCT	GTTGCTTATG	900
GCTGGATATT	GTTATTCAGC	AGATGAATCA	CAAGTTTAGC	CTGAGGGCCC	TAAAGCATCA	960
GAAATAAATT	AGAGCCGAGC	AAAGTTTAAC	TTCTCTGGAA	CTTGCACCTT	TAGTTTCCAT	1020
GTATTTCTGG	AACCAAGATA	TTTCAAAGGC	TTACTTTATT	TCAGACACCT	ATTATCTTCA	1080
AGTCACAGAT	AACTATTGAT	TCTGTAAAGT	GTTTCAAAGA	TTTTTGTTCA	CTAGACATTT	1140
TTAAATTTGT	TCAACTCCTC	CTCATCATT	TAGAAATTAT	TTCTGTTAGG	TAAAATTAAA	1200
ACTAACAATG	TATTTTAGTT	TATTTTCTTA	ATGATACCAG	TCACCTTTCG	GGGCTAACTA	1260
AACATTTTGT	GCAGCATTCT	CTTAGTTTAC	ATCCTCCTTT	CTTTCAGTCT	TCCTGTTTAT	1320
TAAGGCTGTC	CTGTAGCAAA	CAAAAGAGTG	ACTCATGTTA	AAAGTATTTT	AACTGCTCTA	1380
ATATATCTGA	GGAAGAATAA	CTTTCTAAAT	TAAAGTAATG	TATTTTATTA	AATATTAAAA	1440
TGCATTTTTT	GGCTATTCAT	TTCTGTATGT	AAAAGAAAAG	TTAACTTTAT	GGTGTATATG	1500
AAAATATGCT	AAATTTAGAT	TTTAGAGCAA	TATATAGGGA	GATATGTCAC	AAATTTCTAC	1560
ATTTTGGTTA	AATTATTAGT	ATTTTTTTAT	ATTCAAATGT	GCCTTGATAT	TTAAATAATA	1620
TACTGAATGC	AGAATTTATG	TTATGTGAAC	CATTATGGAA	AATGTTAATG	TTAACAAAAT	1680
GAGGTGTATT	GACTTTTCAA	CAATGTAAAT	TAAAGATGGT	ACATCTACTG	TTTAAGGGCA	1740

GAGGAATTAA AAGAGTATAG ATACTGAAAT GTATCACTTA CTAGTAGTGT GGCTATAATC	1800
AAATTAATTA ATCTCTCTCT AGGCTTTAGC TTCCTCATCT TAGTTTGTTT AGGCTACTGT	1860
AACAAAATAA CATAGATTAT GTACTTTTAA ATGACAGAAG TTTATTCGGC ATGGTTTGGG	1920
AGACTAGGAA GTCTAAGATT AAAGAACCAG CAAATTTGGT GTCTGATGAG GACCCATTCC	1980
TTTGTTTACA GATGATGCCT TCTCATTGTG TTTTCAAATG TTAGAAGGAG CTAGCTAGCT	2040
TTCTGGGGTC TCTTTTGTA AGGCACTAAT CCCAGTCATT AGGGCAAATT GGCTCCTACA	2100
GGCCCCACCT ATCTCCTAAT ACCATCACCT TGAGGATTAA GATTCTTACA TATGAATGAA	2160
GCAGGTGTTG TAGAAGGTCA GTCAGTTAGA CCATAGCACC ATCTGTAAAA TTGAATAGTA	2220
ATTTACTGCC TCATTGGATG TCAGGATTAA AGGAGATAAG ATTTTATTAG TTAGTAGTTA	2280
CCATAGTGGT TTTTTTTTTT CACTATAATG TTCGTTTTTT TGTTCATGC TTGTACCTTC	2340
AACATTTTCT TCCATTTGAA TACTTCTTTT GTCTCCTGTA GGCCTGTCTG TCCACTTAGG	2400
TGTAAGATGT GTTTTTGTGT CAGGAATGAT GGTGCAATGC TAATGTTCCA TTGCCCTATT	2460
TGGCAATACT CTGATCATT ACTATAAAGA ATAACACCAG TGTTAACTAA CTCTCCTTGC	2520
CTGACAGTAG TGCTGCCACT ATTCCTTGTT TCTGTGGTAA TAGATGAGGT TTGTATGGTC	2580
CTGTTATTCC AGCCTCCAGA CACCATTCCA GATCAACTGG TGCCYTCWAC GCCCCGAAG	2640
TGTATGGGGC CTCAGGTGAA GGATGAGWAC ATTTTCACTA TCATCTGGCA TTCATCTCAG	2700
ATTTTATCCT TTTCAGTTTC CATTAAATAA TATTCATGTT TTAAAATTGA TTTTTTATTA	2760
TTTAAATTTA ATTTGTTGGA GAATAAACTT TTTTTTTTCT TTTCTCCCAA GTAACGTTTT	2820
CCCCTTTAGC AACTGTATTG AGCATTTTTT TCACTGGTAT ATGGACATTT TTTTGTATAA	2880
CCTGTTGTGT CATTTTTTAAA TATAGAATTG TTTTATGTT CTCATCTTTG TATATATGTT	2940
TAAAAAAAAA AAAAAA	2956

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Lys Pro Phe Ser His Ser Phe Arg Arg Ile Gly Phe Phe Ile
 1 5 10 15
 Ala Ile Leu Phe Thr Tyr Gly Tyr Cys Ile Ala Lys Ala Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCGGGAAA AAAAGCCATG TATTCTTTTCG TTTCTCTCTA AAAGAAGAAA AATATAATTT	60
AAAAATACAT TGC GTATTTT CTAAAACAAT AAATTTATAG TGTTAATATT CATAGGGTCA	120
ATCAAAATGA AGCTTCTCCT TTGGGCCTGC ATTGTATGTG TTGCTTTTGC AAGGAAGAGA	180
CGGTTCCCCT TCATTGGTGA GGATGACAAT GACGATGGTC ACCCACTTCA TCCATCTCTG	240
AATATTCCTT ATGGCATACG GAATTTACCA CCTCCTCTTT ATTATCGCCC AGTGAATACA	300
GTCCCCAGTT ACCCTGGGAA TACTTACACT GACACAGGGT TACCTTCGTA TCCCTGGATT	360
CTAACTTCTC CTGGATTCCC CTATGTCTAT CACATCCGTG GTTTTCCCTT AGCTACTCAG	420
TTGAATGTTT CTCCTCTCCC TCCTAGGGGT TTCCCGTTTG TCCCTCCTTC AAGGTTTTTT	480
TCAGCAGCTG CAGCACCCGC TGCCCCACCT ATTGCAGCTG AGCCTGCTGC AGCTGCACCT	540
CTTACATCCA CACCTGTAGC ATCTGAGCCT GCTGCAGGGG CCCCTGTTGC AGCTGAGCCT	600
GCTGCAGAGG CACCTGTTGG AGCTGAGCCT GCTGCAGAGG CACCTGTTGC AGCTGAGCCT	660
GCTGCAGAGG CACCTGTTGG AGTGGAGCCA GCTGCAGAGG AACCTTCACC AGCTGAGCCT	720
GCTACAGCCA AGCCTGCTGC CCCAGAACCT CACCCTTCTC CCTCTCTTGA ACAGGCAAAT	780
CAGTGAAATT CTCTAGAAGA GTACCATGGG TTCATTTCTA TACTGATGCA GAAATAAGTG	840
AAATCTACAA AAGTTTTCTT TCTTTTCCAA AGACTATTTT ATTCTGTAGT ATTCAGAGTA	900
TTCATCTCAC TACATAGATT TGTTTGTGGT AGTTATTTCC TTGGAATTAA TTTATATTGA	960
AAAAACATTG ATAATTAAAT AAATAAAATA GATAATTTAG ACCAATGGTG ATAAGGTCTG	1020
GATGAAACT ACGCTATGGA GGACTGAAAT GGCAATCATT CAGCCTAGCC TGGAGTCTGA	1080

TTATACAGCT ACTATAGGAT GATGTTAGTA TTGGTTTTGA GTGCAATAGG TTTTTCCTA 1140
 AACAAACATA TTTTGTAGTC AATGAACTTT TTGTCACAAA ACAGTAAAAC ATCTGTGTTT 1200
 AACCTATGGT AAACAACATG TTAATGAACT ATGCTATCCA TGACTTAATG GACAGTTCAA 1260
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 AAAAAA 1325

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Lys	Leu	Leu	Leu	Trp	Ala	Cys	Ile	Val	Cys	Val	Ala	Phe	Ala	Arg	1	5	10	15
Lys	Arg	Arg	Phe	Pro	Phe	Ile	Gly	Glu	Asp	Asp	Asn	Asp	Asp	Gly	His	20	25	30	
Pro	Leu	His	Pro	Ser	Leu	Asn	Ile	Pro	Tyr	Gly	Ile	Arg	Asn	Leu	Pro	35	40	45	
Pro	Pro	Leu	Tyr	Tyr	Arg	Pro	Val	Asn	Thr	Val	Pro	Ser	Tyr	Pro	Gly	50	55	60	
Asn	Thr	Tyr	Thr	Asp	Thr	Gly	Leu	Pro	Ser	Tyr	Pro	Trp	Ile	Leu	Thr	65	70	75	80
Ser	Pro	Gly	Phe	Pro	Tyr	Val	Tyr	His	Ile	Arg	Gly	Phe	Pro	Leu	Ala	85	90	95	
Thr	Gln	Leu	Asn	Val	Pro	Pro	Leu	Pro	Pro	Arg	Gly	Phe	Pro	Phe	Val	100	105	110	
Pro	Pro	Ser	Arg	Phe	Phe	Ser	Ala	Ala	Ala	Ala	Pro	Ala	Ala	Pro	Pro	115	120	125	
Ile	Ala	Ala	Glu	Pro	Ala	Ala	Ala	Ala	Pro	Leu	Thr	Ser	Thr	Pro	Val	130	135	140	
Ala	Ser	Glu	Pro	Ala	Ala	Gly	Ala	Pro	Val	Ala	Ala	Glu	Pro	Ala	Ala	145	150	155	160
Glu	Ala	Pro	Val	Gly	Ala	Glu	Pro	Ala	Ala	Glu	Ala	Pro	Val	Ala	Ala				

165

170

175

Glu Pro Ala Ala Glu Ala Pro Val Gly Val Glu Pro Ala Ala Glu Glu
 180 185 190

Pro Ser Pro Ala Glu Pro Ala Thr Ala Lys Pro Ala Ala Pro Glu Pro
 195 200 205

His Pro Ser Pro Ser Leu Glu Gln Ala Asn Gln
 210 215

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCGGGCTCA CANGAANAGT CTCACCTCAG TGCCAAGGGG TGTCAGAGAT GCTCACTGCC 60

CTCCTCTCCT TGGGGTTGCA TGNAGGCATG ATGGCGCTTG GCCGTGGCAG GGTAAGGAAC 120

CGGCGACNGA GGCCCATCAC GTGTTACAT GCTCTCCTGC GTCNGTGCTT GGGAGATATG 180

GACTGTCNTG TCCTTAGACC ACATTTATNT CAAGGCAAGG GGAGC 225

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GGTTCAAAAT GAGGCAAAGA TAGGAAAGTG CTTCTTACAG ATAATTTTCA AGGCCAGTGA 60

CTGGAGAGAG GGGTAGGTCT GTCAATCGAG TGCTTGCTGA CTGCACATAT CACAGGGCGT 120

GTGACGACTG CTGGGAGAGG AAAGCGAGAC ATCATTCCAA CCCTCCAGAA GCTAAAGATC 180

CTGGAACTCA AGGGGAAAAC TAACGTAAGT GCGAAAGCGA ACAAGCAAAC ATGTCCTCAA 240

CGGGGCAGGC AGGCTGTCGG GGTACAGAGC TGGGATCTGG GAAGGAACAG AGAGGGCCGC 300
 TCAGGGAGAG GAAGCACAGT GCCACCGGAG GCACGCACTC AGCAGGCACT CGCAGGCTGG 360
 GCAGAGGTAG AGAAGCAGCG CTGCACAGGC AGGCAGCTGA CCCAGGGCTC TTAGAGCCGG 420
 GCAGGAGAGC TGGTGTGGGA CCTGGGAGGA GGACAGGAGC CTTCAAAGCA GCACCGCCTG 480
 ATTGCAGCCA GGAGGGTAGC ATCAAGGAAG ATGGAAGTGC GGCCAGGCCA CAT 533

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ser	Ser	Thr	Gly	Gln	Ala	Gly	Cys	Arg	Gly	Thr	Glu	Leu	Gly	Ser
1				5				10						15	
Gly	Lys	Glu	Gln	Arg	Gly	Pro	Leu	Arg	Glu	Arg	Lys	His	Ser	Ala	Thr
			20					25					30		
Gly	Gly	Thr	His	Ser	Ala	Gly	Thr	Arg	Arg	Leu	Gly	Arg	Gly	Arg	Glu
		35					40					45			
Ala	Ala	Leu	His	Arg	Gln	Ala	Ala	Asp	Pro	Gly	Leu	Leu	Glu	Pro	Gly
		50				55					60				
Arg	Arg	Ala	Gly	Val	Gly	Pro	Gly	Arg	Arg	Thr	Gly	Ala	Phe	Lys	Ala
65					70					75				80	
Ala	Pro	Pro	Asp	Cys	Ser	Gln	Glu	Gly	Ser	Ile	Lys	Glu	Asp	Gly	Thr
			85						90					95	
Ala	Ala	Arg	Pro	His											
			100												

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TAGGCAGTCA TCTTTGTAAA CCTCCACTGG TGCTGGCTGC GTTTAGAACA TACTCCATAT	60
AAACAGGCC CTGGGATTAC AGGCATGAGC TACCGTGCCT GGCCCCCTTT TTTTAAATTA	120
CAGAGAAATA AGTTACACCT TAGTATCAGA TATTAATTTT CTTCAGTGTT CAGGCAATTA	180
GTATTTAGAA AGCTCTTGTC ATGAGATGGC TCTGGGATGT GATGATGATT GTTGGGATTG	240
AAAAAATGGT AGTATCATGG AGAGATCATA ATAAATTCTT AGTATTAAAA GTGGTTTTGC	300
TTTCAGTTAG GGAGAAAAAT TAGATTGTAC TATTTTTCCT CTATGATTTC CTTCAGTTAT	360
CTTCCAAATG TTGTTTTTTC CCCACAGCCC CCTTAACATT GTTCTCTATG CACTTCTCAA	420
TACATTTTCA TTTGTTTCTC AAAAAAAAAA AAAAAAAA	458

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTTTTTTTTT TTTTGTAGA GACAGGGTCT TGCCATTTTG CCCAGGTTGG TCTCAAACCT	60
CTGAGCTCAG GCTATCTGCC CACCTTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC	120
CACTGTGCCC GGCCTGTATT GTTTAAGTT AACTTATTC CTTTAAAAAT TCAGAATTTG	180
TTAAGCATTT AAAACAAATT CATAAATTAA AACCTCCTTG AGATACCATT TACCATGTAG	240
TTTGATGAAC ATAATACATG GTGCATTACA TTGGCAAAAG CAGTGGGGAA AAAGATGCTT	300
TTATAAATGT CTGGTGGGAG TTAAATTGTG TAACTTCTAT TAACTTTTG TAATAGCTAC	360
CAAAATATGT TATTTCTATC TACCTCTCTC TCTCTGACTC AACAGTTCCA TTTCTAGGTT	420
TTGTGTTGTG GATATTCTTG AACATTGTGA AATGTATACA GGGAGGCTTC ACAGCAGCAC	480
TGTTTGTTC AAATGATTTG AAAACAACCT CTCCATAAAC GAGATAGGCT AAATCAAGCA	540
TGGCACACCT ATACAATGGA TCGGCCATT AAAAAGAACA AGGCAGCTCA TATGCATCAA	600
TATAAAAAGG TCTATAAACT ATACTATCAA ATGAAAATAG CAAGATGCTA CCATTTATAT	660
TAAAAGAGG ACAAATATT AATATATTCA TGTTGCTTG TCTATGTGGA ATATTTCTGG	720

ATATATACAT AAGAAGTTAC ATTGGTTACC TATGGGCAGG TTACTACTGG GTGGCTTG TG 780
 GGTGAGGGCA GGAAGAGCTT ACTTTCCATG GTAAACCTTT TTGTATATTT TGCAGCATTC 840
 AAAAATTCTA ATTTAAAGTT TATTTT TAGAA AAATGCCCCC ATGTATACAA GTGATTTCCA 900
 AGTTCCTCCT TCAATATTTT TAATGATTAT GGAACACACT GAACTTCTTT TTTATTATTC 960
 TAGCTGTGAA CTCTGTCTGC TGTCTACATG CACATATATA ATCTATGTAA TATTTAAATT 1020
 TATATCCTTT ATATGTCAGT TGGGTGGTGA GTAAAAGAAA AATATATTTT TATCAGCAAA 1080
 CTTGGTAAAT TGTTGAGGTT TCTGATATAG TCAGAGGTAG TTGCTTATCA CAACATTAGG 1140
 TAAGTTTTTA AARACACCTA TTTAAAACAC ACTGATGTAT ATATATATTG GTCTGTTTTTC 1200
 ATGCTGCTGA TAAAGACATA TCCAAGACTG GGAAGAAAAA GAGGTTTAAT TGGGCTTATA 1260
 GTTCCACATG GCTGGGGAGG CCTCAGAATC ATTGCGGGAG GCAAAAGGCA CTTCTTACAT 1320
 GGCAGTGGCA AGAGAAAAAA AAAAAAAAAA 1350

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Leu	Pro	Phe	Ile	Leu	Lys	Arg	Gly	Gln	Asn	Ile	Asn	Ile	Phe	Met
1				5				10						15	
Val	Ala	Cys	Leu	Cys	Gly	Ile	Phe	Leu	Asp	Ile	Tyr	Ile	Arg	Ser	Tyr
			20					25					30		
Ile	Gly	Tyr	Leu	Trp	Ala	Gly	Tyr	Tyr	Trp	Val	Ala	Cys	Gly		
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCGGGACACT	ACATGAAGTC	CTGAAAATAA	CAGAGAAACT	GTTATATCTT	TTTAATGATT	60
TATTTGCAAG	TATTGAGGTT	GACCTGAAAA	ACAATGAAAC	ACATGAACAC	ACTTCCGATT	120
TTCTCCTCGC	TGATTAGCTT	CCTGCCTGCT	GTCAGTGCTG	GACGAAGTGC	TATAACTACT	180
TTATGTAACA	TTACAGAACA	GCTAGAGGTC	CTGGGGTAAG	AGAAAAAAG	CACATCACAA	240
CAAATGTGAA	AGCCTTCATT	ATTACACGTT	CCAGTTTGTC	TCGCTGTGTA	GGCATAAGCT	300
AATGGTTTAT	TTTCAGAAAG	CTGCCTGAAA	CGTTGCTTTG	TATTCTTCTA	GGAAGAACTT	360
TAATTCCTCC	TGAGGAACTC	TACTTTCTGA	GCCAAACTGC	TAATTTTCTG	CGGAACTGTC	420
TAGAAGATCA	TTCAAGAGAC	CCTGCAGTTG	CACTTTCTCG	TAAAAGTTAA	AAAAAAAAAA	480
AAAAAAAAAAG	GTTTTTCCCG	GCCTTTGAAC	ATTTTGCTTA	TGAGAGTTTT	GCATATATTT	540
TATACTTGAG	TAGACAACTT	TAATAATCCA	TATTTATACT	ATCGCAGAAG	TAAGCATTTG	600
GCAAACGTTT	AGCCATTAGC	ACTCATTTAA	CCCTGTTAGC	AATATTCTTT	TGAAAAAAGT	660
GCCAGTCCTT	ATGTGATAAA	CTAAGAAGCC	CATTGAATAT	AAAANTGTGT	NGGACTGAAA	720
CNGTGACCTT	ATATTATTGC	TAAGGGAATA	TGAGATTAAAC	TTCCTACAGG	GGCCANAACC	780
ANANAAAGGC	TTCCAGCAAC	TTCGATNAAA	NTANTTTGGC	CACATNTCAA	GCCAATTGTT	840
TGTACTATTT	ATGTACCTTT	TTCATAACTG	GAATTGCCAA	ATAAGCATGG	AGATCTAAAT	900
GRAAAAAAAA	AAAAAAAAAA	AAAGCGGCCG	CAGGTCTAGA	ATTCAATCGG	AAAAAACAAA	960
GAGAAGAAAC	ATACTGCCCC	ATCTTGTTTG	CATGAAACTC	TAGAATCTGG	TGTTTCTCTA	1020
TTTATCTGCT	CCCTCTTTGC	CTACCTTGGN	ATTTCTTTTT	TTTTTCTTTT	GTAAGTATGG	1080
TTTTTACCTA	AAGTTTAAAC	TTTTTATTAT	TATTTTCTCT	CTAAATCTTT	GCTAGTTAAT	1140
AACATTATTA	ACTTCAAGAT	TTTAGAAGAG	CAGTGATGAT	AGTAATGATC	GATAACTAGA	1200
CTATCGAGTT	TCAGAAGAAA	CTTCCAAGTA	TATATAATGT	TTGACATAGC	CTTTATTTCT	1260
ACAAATCTAC	TACCTGTAAA	CTAACATTTT	AAAATACCTG	TATATGGCTG	GGTGTGGTGG	1320
CTTACACCTG	TAATCCCAGC	AGTTTGGGAG	CCTGAGGTGG	GCAGATTGCT	TGAGCCCAGG	1380
AGTTGGAGAC	AAGCCTGGAC	AAAATAGACC	TCTCTCTACA	AAAAGTACAA	AAAATTGGCT	1440
GGGTGTGGTG	GCACACGCCT	GTGGTCCCAG	CTACTCGGGA	GGCTGAGGTG	GGAGGATTGC	1500
CTGAGCCCGG	GAGATGGTGG	TTGCAGTGAG	CTGAGATCAC	CCCATTGCAC	TCCAGCCTGG	1560
ATAACAGAAT	AAGATGCTGT	CTTAAAAAAA	AAAAAAAAAA			1598

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Lys His Met Asn Thr Leu Pro Ile Phe Ser Ser Leu Ile Ser Phe
1 5 10 15

Leu Pro Ala Val Ser Ala Gly Arg Ser Ala Ile Thr Thr Leu Cys Asn
 20 25 30

Ile Thr Glu Gln Leu Glu Val Leu Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCGTCC AGGTCTAAGC GGC GTGCCGT GGAAAGTGGG GTTCCGCAGC CGCCGGATCC 60
CCCAGTCCAG CGCGACGAGG AAGAGGAAAA AGAAGTCGAA AATGAGGATG AAGACGATGA 120
TGACAGTGAC AAGGAAAAGG ATGAAGAGGA CGAGGTCATT GACGAGGAAG TGAATATTGA 180
ATTTGAAGCT TATTCCCTAT CAGATAATGA TTATGACGGA ATTAAGAAAT TACTGCAGCA 240
GCTTTTTTCTA AAGGCTCCTG TGAACACTGC AGAACTAACA GATCTCTTAA TTCAACAGAA 300
CCATATTGGG AGTGTGATTA AGCAAACGGA TGTTTCAGAA GACAGCAATG ATGATATGGA 360
TGAAGATGAG GTTTTTGGTT TCATAAGCCT TTAAATTTA ACTGAAAGAA AGGGTACCCA 420
GTGTGTTGAA CAAATTCAAG AGTTGGTTMT ACGCTTCTGT GAGAAGAAGT GTGAAAAGAG 480
CATGGTTGAA CAGCTGGACA AGTTTTTAAA TGACACCACC AAGCCTGTGG GCCTTCTCCT 540

AAGTGAAAGA TTCATTAATG TCCCTCCACA GATCGCTCTG CCCATGTACC AGCAGCTTCA 600
 GAAAGAAGCTG KCGGGGGCAC ACAGAACCAA TAAGCCATGT GGGAAAGTGCT ACTTTTACCT 660
 TCTGATTAGT AAGACATTTG TGGAAGCAGG AAAAAACAAT TCCAAAAAGA AACCTAGCAA 720
 CAAAAAGAAA GCTGCGTTAA TGTTTGCAAA TGCAGAGGAA GAATTTTCT ATGAGAAGGC 780
 AATTCTCAAG TTCAACTACT CAGTGCAGGA GGAGAGCGAC ACTTGTCTGG GAGGCAAATG 840
 GTCTTTTGAT GACGTACCAA TGACGCCCTT GCGAACTGTG ATGTTAATTC CAGGCGACAA 900
 GATGAACGAA ATCATGGATA AACTGAAAGA ATATCTATCT GTCTAACCCA TTTCCAATGG 960
 ACAGTGATGG GCTTGTTTTT GTAAAATTAC CAGAAAACCTC AGTGGAGATT TACTGAAAAA 1020
 CTCAGACTTT ATTCAGATTA AGTTCCTCTA CAAAAGTAG GGTCTGTCC CATGTGTYTC 1080
 TGACACATTT ACAAATACC AGTTTTTTAA AATTTTGGTC AAATTATGAG TGGTTGATTT 1140
 AAAAAGCTTT CCAAGAAGAA GAAAAGCATG GAGTAGTAAT TTAAAGAACT CAATAAAAC 1200
 TTCTATTTTT TATTTTAAAA TAATAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1257
 (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met	Ala	Ser	Arg	Ser	Lys	Arg	Arg	Ala	Val	Glu	Ser	Gly	Val	Pro	Gln	1	5	10	15
Pro	Pro	Asp	Pro	Pro	Val	Gln	Arg	Asp	Glu	Glu	Glu	Glu	Lys	Glu	Val	20	25	30	
Glu	Asn	Glu	Asp	Glu	Asp	Asp	Asp	Asp	Ser	Asp	Lys	Glu	Lys	Asp	Glu	35	40	45	
Glu	Asp	Glu	Val	Ile	Asp	Glu	Glu	Val	Asn	Ile	Glu	Phe	Glu	Ala	Tyr	50	55	60	
Ser	Leu	Ser	Asp	Asn	Asp	Tyr	Asp	Gly	Ile	Lys	Lys	Leu	Leu	Gln	Gln	65	70	75	80
Leu	Phe	Leu	Lys	Ala	Pro	Val	Asn	Thr	Ala	Glu	Leu	Thr	Asp	Leu	Leu	85	90	95	

Ile	Gln	Gln	Asn	His	Ile	Gly	Ser	Val	Ile	Lys	Gln	Thr	Asp	Val	Ser	100	105	110
Glu	Asp	Ser	Asn	Asp	Asp	Met	Asp	Glu	Asp	Glu	Val	Phe	Gly	Phe	Ile	115	120	125
Ser	Leu	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Gly	Thr	Gln	Cys	Val	Glu	Gln	130	135	140
Ile	Gln	Glu	Leu	Val	Xaa	Arg	Phe	Cys	Glu	Lys	Asn	Cys	Glu	Lys	Ser	145	150	155
Met	Val	Glu	Gln	Leu	Asp	Lys	Phe	Leu	Asn	Asp	Thr	Thr	Lys	Pro	Val	165	170	175
Gly	Leu	Leu	Leu	Ser	Glu	Arg	Phe	Ile	Asn	Val	Pro	Pro	Gln	Ile	Ala	180	185	190
Leu	Pro	Met	Tyr	Gln	Gln	Leu	Gln	Lys	Glu	Leu	Xaa	Gly	Ala	His	Arg	195	200	205
Thr	Asn	Lys	Pro	Cys	Gly	Lys	Cys	Tyr	Phe	Tyr	Leu	Leu	Ile	Ser	Lys	210	215	220
Thr	Phe	Val	Glu	Ala	Gly	Lys	Asn	Asn	Ser	Lys	Lys	Lys	Pro	Ser	Asn	225	230	235
Lys	Lys	Lys	Ala	Ala	Leu	Met	Phe	Ala	Asn	Ala	Glu	Glu	Glu	Phe	Phe	245	250	255
Tyr	Glu	Lys	Ala	Ile	Leu	Lys	Phe	Asn	Tyr	Ser	Val	Gln	Glu	Glu	Ser	260	265	270
Asp	Thr	Cys	Leu	Gly	Gly	Lys	Trp	Ser	Phe	Asp	Asp	Val	Pro	Met	Thr	275	280	285
Pro	Leu	Arg	Thr	Val	Met	Leu	Ile	Pro	Gly	Asp	Lys	Met	Asn	Glu	Ile	290	295	300
Met	Asp	Lys	Leu	Lys	Glu	Tyr	Leu	Ser	Val							305	310	

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGTCCTGC	CACACAAGCT	GGGCGGCGGA	GGCCACGCAG	CCGGGCCTTC	TTCTCTCTGG	60
GACCCTCCGC	CAGCGCATAG	CCGCAGGCCG	GTGTGACTTC	TGCACCCTCG	GTTCTGAGGG	120
TACGGTGACC	CCTAGTGGGC	AGTTTGCAAA	ATGTGATTCC	TTCTTCCCAA	CTCCCCATCC	180
CCCCTTCCCT	TCCCGTCACG	TCCTGTTTGG	GGGTTAATTC	GGTTTTTTCT	CTGTTGCATC	240
GCGCCTACTG	TGCGTGTGCG	ATARCGTGTG	TGGGGGTGAG	AGTTTGTTTT	CTGGAATGGT	300
AGGTGCTGGG	AGGAGGAGTT	TGATGGAGGG	CTTCCTGGCT	GCTTCTGGCC	CTCACCTCGT	360
GGAGGCCTTC	ACAGAGACCC	TGTGGGCCCT	GGCCCTGTGC	TGGCACTGTG	CCAGTCATGA	420
GGCAGCTCTG	ATCACTTCCC	CACTGTGGAA	ACAGGACTGA	CCCAGCCTTC	AGTGTGGGCT	480
GCTGAAGCTA	TCCTCCTCAG	GCCTCAGGGA	TGACCTCCTG	CCTGAGCCTC	TCACAGGCTG	540
GCTGTGGGCC	AGTTTCATCT	GCTTTCCTGT	TGGGGGTCCC	GGGCCCTCTG	TGTCCTTGAC	600
CCACTGGTGT	TCTGTGCAAG	GCTTCTTCCC	ATTACCAAG	TGCACACCTT	GCATCTGCCG	660
CTCGGCATGC	ACCAGTTCCA	CACACCATCC	CATTTTACAG	ACAAGGACGC	TGAGGCCTGC	720
AGCAGCAGTG	TGACTTGCTC	AAGGTCCAGT	GAGTGACCTC	ATTCCCAGA	AAAGGCTCCT	780
CCCACACCAG	AGTACAGCCT	GGGTAGGGGG	AAAATCAGTT	CTTTCAGCTA	CCACCCATCC	840
AACCTTTGGG	CCTATGTGAA	AAGAAAGGAA	CTAAGCTGGG	TGTGTTCTGT	CTGGACCTGG	900
GGAGGCCCT	GAAGGCAAAG	AGGGAAACTG	TCCCAGCTGT	TCTGTCCTAG	GGGAGGGGGA	960
CATAGCCCTA	GCAGGAGCTC	CCAGCCCCTC	TTGGCACTCT	GACACACAAG	TACACCCATC	1020
TGGGGCCCGC	TTTGCCACGA	AGAGCTGGGC	AGGCCTGCAG	GGTGTGGGGA	AGGAGGACAC	1080
AACCTCAAGA	AAGGAAGCGT	GAACCCAGG	GAACAGCGGG	TCCCTTCCCT	CCTCAGACAC	1140
AAGCCACCTC	AGCTTGTGGC	TCTTGCCCC	CAGCCCCACC	AACCCACCTG	TTCATTTATT	1200
CAACAGACAA	TGACAGCTGA	TATTTATTGG	ACATTTGCAC	CATGCCAAGC	ATTCGGCTTG	1260
GATTATCCCA	TTTGTTTCTC	ACAGCCGGTA	TTTATTGTCT	GCTCCTCTGT	GCCAGGTGCT	1320
GTGCTCTGGG	CAGGGGCACT	GCATGGGCTG	CCTGCCCTGG	TGGAGCTTGT	GGTCTGATGG	1380
GTGAGGCTGA	CCCAAGCCCA	CCCCATTGCC	AACAGGGCCA	GGGCAAGAGT	ACACACAGGG	1440
GCCTCATACC	ATATGTCTAA	ATATTTAAAA	GTTATCAATC	AAGCTAACAA	CTGTTAAATA	1500
AAATATGTTC	TATTCTCCTA	CTTTGAAAAA	AAAAAAAAAA	AAAA		1544

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

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Met Pro Ser Ile Arg Leu Gly Leu Ser His Leu Phe Leu Thr Ala Gly
1           5           10           15

Ile Tyr Cys Leu Leu Leu Cys Ala Arg Cys Cys Ala Leu Gly Arg Gly
20           25           30

Thr Ala Trp Ala Ala Cys Pro Gly Gly Ala Cys Gly Leu Met Gly Glu
35           40           45

Ala Asp Pro Ser Pro Pro His Cys Gln Gln Gly Gln Gly Lys Ser Thr
50           55           60

His Arg Gly Leu Ile Pro Tyr Val
65           70

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(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CNATGCAGGTC TAACTCCTCC ACTCTGGG

29

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNAGTTTGGTG CTCTGCTCTG ATATTGAC

29

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GNCATCAATAT CCTTACGGTC TCCGAAGC

29

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAAATAGGAA CTTTCATGAG AATCAGGA

29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ANACAATGCAG GCCCAAAGGA GAAGCTTC

29

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNTTGCTTGTT CGCTTTCGCA CTTACGTT

29

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucelotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANTGGTAGCAT CTTGCTATTT TCATTTGA

29

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TNGGAAGTGTG TTCATGTGTT TCATTGTT

29

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNCCTCGTCCT CTTTCATCCTT TTCCTTGT

29

- (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANCACCTGGCA CAGAGGAGCA GACAATAA

29

- (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGAGCCTT TGAGGGGAAC GACTTGTCGG AGCCCTAACC AGGGGTATCT CTGAGCCTGG 60
 TGGGATCCCC GGAGCGTCAC ATCACTTTCC GATCACTTCA AAGTGTAAGG GGGGCCCTAC 120
 TGACCCTTGG AATTTAGGGG GGCTACCCTA GGCGGCATCC ACAACAGAGA GAATTCCTTT 180
 GGAGAGGGGA CCCTGGTGCT CGGCTGTCCC TCTCATCCGC GTAGAAAGTC CCTCATCTGG 240
 GGGCTCCCGA ACTCAGCCCT CTCACATTGT GGCCGGCTTT ACTGACCCTC ACAGACCCAG 300
 GCTGGGCCCT CCCGATAGAG GCCAGCCAAA GGTTCACCTA GCCTCTCTTT CAAGGCTGGT 360
 GTATCTCTAA ATCTTAGACC CTCCTCCGTT ACCGTCAGCC AGGTGGGATG CCCACGTTTT 420
 GGAGAGAAAC CGTTCTGAGG AACCCGGGCC TCTGGGTCCC AGCTGGCTCT CCGGCCCCCA 480
 GGTTATGTAT TCTGGGTGGG CCACAAACAG TGGAATTCTA GGCACTCCCG GGACAGGGTG 540
 GGAAGTGTGT CCTCATTCAT GCAACCAGCA AATATTCACG GCACCTTGTT TGTGCCAGAC 600
 AGCAGACCGA GGACACGGTT GTTACCAAGA CCAGGCTGTT GCCTTGGAAG AGCCAGAGC 660

GTGTCAAGGG AGACAGCCAC ATCACGCCAG AAATACATGA CAGCTGGATT AGCCCTGGGA 720
GAGGGAGGCC CAGATGTGGG AGCTCAGGGG AGGTGCAGCT CAACGTGGAG TTTGGAGGAG 780
GCTACCTTGA CCTTTGAATG CCAAGTGGGA GCCAGCCAGA TGAAAGGGGT TAAAACTAA 840
TATTTATATG ACAGAAGAAA AAGATGTCAT TCCGTAAAGT AAACATCATC ATCTTGGTCC 900
TGGCTGTTGC TCTCTTCTTA CTGGTTTTGC ACCATAACTT CCTCAGCTTG AGCAGTTTGT 960
TAAGGAATGA GGTTACAGAT TCAGGAATTG TAGGGCCTCA ACCTATAGAC TTTGTCCCAA 1020
ATGCTCTCCG ACATGCAGTA GATGGGAGAC AAGAGGAGAT TCCTGTGGTC ATCGCTGCAT 1080
CTGAAGACAG GCTTGGGGGG GCCATTGCAG CTATAAACAG CATTTCAGCAC AACACTCGCT 1140
CCAATGTGAT TTTCTACATT GTTACTCTCA ACAATACAGC AGACCATCTC CGGTCCTGGC 1200
TCAACAGTGA TTCCCTGAAA AGCATCAGAT ACAAATTGT CAATTTTGAC CCTAACTTT 1260
TGGAAGGAAA AGTAAAGGAG GATCCTGACC AGGGGGAATC CATGAAACCT GTGATATTCT 1320
TGCCCTTTAC AATACAGCAC TGAAGCCAGG ACATGCAGCT GCATTTTCAG AAGATTGTGA 1380
TTCAGCCTCT ACTAAAGTTG TCATCCGTGG AGCAGGAAAC CAGTACAATT ACATTGGCTA 1440
TCTTGACTAT AAAAAGGAAA GAATTCGTAA GCTTTCCATG AAAGCCAGCA CTTGCTCATT 1500
TAATCCTGGA GTTTTTGTG CAAACCTGAC GGAATGGAAA CGACAGAATA TAACTAACCA 1560
ACTGGAAAAA TGGATGAAAC TCAATGTAGA AGAGGGACTG TATAGCAGAA CCCTGGCTGG 1620
TAGCATCACA ACACCTCCTC TGCTTATCGT ATTTTATCAA CAGCACTCTA CCATCGATCC 1680
TATGTGGAAT GTCCGCCACC TTGGTTCAG TGCTGGAAAA CGATATTCAC CTCAGTTTGT 1740
AAAGGCTGCC AAGTTACTCC ATTGGAATTG ACATTTGAAG CCATGGGGAA GGACTGCTTC 1800
ATATACTGAT GTTTGGGAAA AATGGTATAT TCCAGACCCA ACAGGCAAAT TCAACCTAAT 1860
CCGAAGATAT ACCGAGATCT CAAACATAAA GTGAAACAGA ATTTGAACTG TAAGCAAGCA 1920
TTTCTCAGGA AGTCCTGGAA GATAGCATGC GTGGGAAGTA ACAGTTGCTA GGCTTCAATG 1980
CCTATCGGTA GCAAGCCATG GAAAAAGATG TGTCAGCTAG GTAAAGATGA CAACTGCCC 2040
TGTCTGGCAG TCAGCTTCCC AGACAGACTA TAGACTATAA ATATGTCTCC ATCTGCCTTA 2100
CCAAGTGTTC TCTTACTACA ATGCTGAATG ACTGGAAAGA AGAACTGATA TGGCTAGTTC 2160
AGCTAGCTGG TACAGATAAT TCAAACTGC TGTGGTTTTT AATTTTGTA CCGTGGCCCT 2220
GATCTGTAAT TAAAACTTAC ATTTTTCAT AGGAAAAAAA AAAAAAAAAA A 2271

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val Ala
1 5 10 15
Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser Ser Leu
20 25 30
Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro Gln Pro Ile
35 40 45
Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp Gly Arg Gln Glu
50 55 60
Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp Arg Leu Gly Gly Ala
65 70 75 80

Ile Ala Ala Ile Asn Ser Ile Gln His Asn Thr Arg Ser Asn Val Ile
85 90 95

Phe Tyr Ile Val Thr Leu Asn Asn Thr Ala Asp His Leu Arg Ser Trp
100 105 110

Leu Asn Ser Asp Ser Leu Lys Ser Ile Arg Tyr Lys Ile Val Asn Phe
115 120 125

Asp Pro Lys Leu Leu Glu Gly Lys Val Lys Glu Asp Pro Asp Gln Gly
130 135 140

Glu Ser Met Lys Pro Val Ile Phe Leu Pro Phe Thr Ile Gln His
145 150 155

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCGACCGAA GAGGCTGGAC ATGACACCAG TGGCATATCA CGGCCATGGG GTCTCAGCAT 60
TCCGCTGCTG CTCGCCCCCTC CTCCTGCAGG CGAAAGCAAG AAGATGACAG GGACGGTTTG 120
CTGGCTGAAC GAGAGCAGGA AGAAGCCATT GCTCAGTTCC CATATGTGGA ATTCACCGGG 180
AGAGATAGCA TCACCTGTCT CACGTGCCAG GGGACAGGCT ACATTCCAAC AGAGCAAGTA 240
AATGAGTTGG TGGCTTTGAT CCCACACAGT GATCAGAGAT TGCGCCCTCA GCGAACTAAG 300
CAATATGTCC TCCTGTCCAT CCTGCTTTGT CTCCTGGCAT CTGGTTTGGT GGTTTTCTTC 360
CTGTTTCCGC ATTCAGTCCT TGTGGATGAT GACGGCATCA AAGTGGTGAA AGTCACATTT 420
AATAAGCAAG ACTCCCTTGT AATTCTCACC ATCATGGCCA CCCTGAAAAT CAGGAACTCC 480
AACTTCTACA CGGTGGCAGT GACCAGCCTG TCCAGCCAGA TTCAGTACAT GAACACAGTG 540
GTGAATTTTA CCGGGAAGGC CGAGATGGGA GGACCGTTTT CCTATGTGTA CTTCTTCTGC 600
ACGGTACCTG AGATCCTGGT GCACAACATA GTGATCTTCA TGCGAACTTC AGTGAAGATT 660
TCATACATTG GCCTCATGAC CCAGAGCTCC TTGGAGACAC ATCACTATGT GGATTGTGGA 720
GGAAATTCCA CAGCTATTTA ACAACTGCTA TTGGTTCTTC CACACAGCGC CTGTAGAAGA 780
GAGCACAGCA TATGTTCCCA AGGCCTGAGT TCTGGACCTA CCCCCACGTG GTGTAAGCAG 840
AGGAGGAATT GGTTCACTTA ACTCCCAGCA AACATCCTCC TGCCACTTAG GAGGAAACAC 900
CTCCCTATGG TACCATTTAT GTTTCTCAGA ACCAGCAGAA TCAGTGCCTA GCCTGTGCC 960
AGCAAATAGT TGGCACTCAA TAAAGATTG CAGAATTTAA TACAGATCTT TTCAGCTGTT 1020
CTTAGGGCAT TATAAATGGA AATCATAACG TGTTTCTAGG TTATCAAACC ATGGAGTGAT 1080
GTGGAGCTAG GATTGTGAGT GACCTGCAGG CCATTATCAG TGCCTCATCT GTGCAGAAGT 1140
GGCAGCAGAG AGGGACCATC CAAATACCTA AGAGAAAACA GACCTAGTCA GGATATGAAT 1200
TTGTTTCAG TGTTCCTCAA GGCCTGGGAG CTTTTTGAAA AGAAAGAAAA AAGTGTGTTG 1260
GCTTTTTTTT TTTTGTAGAA GTTAGAATTG TTTTACCATA GAGTCTATGT GGGGCTTGAT 1320
TCACCCTTCA TCCATTGGCT GGAACATGGA TTGGGGATTT GATAGAAAAA TAAACCCTGC 1380
TTTTGATTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 1425

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
1 5 10 15
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
20 25 30
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
35 40 45
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
50 55 60
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
65 70 75 80
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
85 90 95
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
100 105 110
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
115 120 125
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
130 135 140
Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
145 150 155 160
Tyr Met Asn Thr Val Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly
165 170 175
Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val
180 185 190
His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile
195 200 205
Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys
210 215 220
Gly Gly Asn Ser Thr Ala Ile

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTTCCAAAGA GCGACTCTTA CTGTTTCTCA TGGTGAGAAG ACAATATTTG CTTTCTCTTT	60
TTCCTTTCTT CCGGATGAGA GGCTAAGCCA TAATAGAAAG AATGGAGAAT TATTGATTGA	120
CCGTCTTTAT TCTGTGGGCT CTGATTCTCC AATGGGAATA CCAAGGGATG GTTTTCCATA	180
CTGGAACCCA AAGGTAAAGA CACTCAAAGA CAGACATTTT TGGCAGAGCA TAGATGAAAA	240
TGGCAAGTTC CCTGGCTTTC CTTCTGCTCA ACTTTCATGT CTCCCTCCTC TTGGTCCAGC	300
TGCTCACTCC TTGCTCAGCT CAGTTTTCTG TGCTTGGACC CTCTGGGCCC ATCCTGGCCA	360
TGGTGGGTGA AGACGCTGAT CTGCCCTGTC ACCTGTTCCC GACCATGAGT GCAGAGACCA	420
TGGAGCTGAA GTGGGTAAGT TCCAGCCTAA GGCAGGTGGT GAATGTGTAT GCAGATGGAA	480
AGGAAGTGGA AGACAGGCAG AGTGCACCGT ATCGAGGGAG AACTTCGATT CTGCGGGATG	540
GCATCACTGC AGGGAAGGCT GCTCTCCGAA TACACAACGT CACAGCCTCT GACAGTGGAA	600
AGTACTTG TG TTATTTCCAA GATGGTGA CT TCTATGAAAA AGCCCTGGTG GAGCTGAAGG	660
TTGCAGCACT GGGTTCTAAT CTTACGTCG AAGTGAAGGG TTATGAGGAT GGAGGGATCC	720
ACCTGGAGTG CAGGTCCACC GGCTGGTACC CCCAACCCCA AATACAGTGG AGCAACGCCA	780
AGGGAGAGAA CATCCCAGCT GTGGAAGCAC CTGTGGTTGC AGACGGAGTG GGCCTATATG	840
AAGTAGCAGC ATCTGTGATC ATGAAAGGCG GCTCCGGGGA GGGTGTATCC TGCATCATCA	900
GAAATCCCT CCTCGGCCTG GAAAAGACAG CCAGCATTTT CATCGCAGAC CCCTTCTTCA	960
GGAGCGCCCA GCCCTGGATC GCAGCCCTGG CAGGGACCCT GCCTATCTTG CTGCTGCTTC	1020
TCGCCGGAGC CAGTTACTTC TTGTGGAGAC TACAGAAGGA AATAACTGCT CTGTCCAGTG	1080
AGATAGAAAG TGAGCAAGAG ATGAAAGAAA TGGGATATGC TGCAACAGAG CGGGAAATAA	1140
GCCTAAGAGA GAGCCTCCAG GAGGAACTCA AGAGGAAAAA AATCCAGTAC TTGACTCGTG	1200

GAGAGGAGTC TTCGTCCGAT ACCAATAAGT CAGCCTGATG CTCTAATGGA AAAATGGCCC 1260
TCTTCAAGCC TGCCTGATTT TTCCTGCATG GGAAGAGCGC ACATGTNGCC CTGAGGTTCC 1320
CTTCCCAGGA CNGCTCCAGG ATCGAGATCA CTGTGAGTGG TTGTGGAGTT AAGACCCCTA 1380
TGGACTCCTT CCCAGCTGAT TATCAGAGCC TTAGACCCAG CACTCCTTGG ATTGGCTCTG 1440
CAGAGTGTCT TGGTTGAGAG AATAACGTTG CAGTTCCCAC AGGGCATGTG ACTTTGAAAG 1500
AGACTAAAGG CCACACTCTG TTAATAATGG GGCACATATG TGTTCCCACC CCACAAATGT 1560
GATAAGTGAT CGTGCAGCCA GAGCCAGCCT TCCTTCAGTC AAGGTTTCCA GGCAGAGCAA 1620
ATACCCTAGA GATTCTCTGT AATATTGGTA ATTTGGATGA AGGAAGCTAG AAGAATTACA 1680
GGGATGTTTT TAATCCCACT ATGGACTCAG TCTCCTGGAA AAGGATCTGT CCACTCCTGG 1740
TCATTGGTGG ATGTTAAACC CATATTCCTT TCAACTGCTG CCTGCTAGGG AAAACTGCTC 1800
CTCATTATCA TCACTATTAT TGCTCACCAC TGTATCCCCT CTACTGGGCA AGTGCTTGTC 1860
AAGTTCTAGT TGTTCAATAA ATTTGTTAAT AATGCTGAAA AAAAAAAAAA AAAAAAAAAA 1920
A 1921

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Lys	Met	Ala	Ser	Ser	Leu	Ala	Phe	Leu	Leu	Leu	Asn	Phe	His	Val
1				5					10					15	
Ser	Leu	Leu	Leu	Val	Gln	Leu	Leu	Thr	Pro	Cys	Ser	Ala	Gln	Phe	Ser
			20					25					30		
Val	Leu	Gly	Pro	Ser	Gly	Pro	Ile	Leu	Ala	Met	Val	Gly	Glu	Asp	Ala
		35					40					45			
Asp	Leu	Pro	Cys	His	Leu	Phe	Pro	Thr	Met	Ser	Ala	Glu	Thr	Met	Glu
		50				55					60				
Leu	Lys	Trp	Val	Ser	Ser	Ser	Leu	Arg	Gln	Val	Val	Asn	Val	Tyr	Ala
65					70					75				80	
Asp	Gly	Lys	Glu	Val	Glu	Asp	Arg	Gln	Ser	Ala	Pro	Tyr	Arg	Gly	Arg

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

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AATGGTTCCA GCCTTAATGG AGAAGCCAGT TTCTTTTTTC TTGTTGTTTT ATTGTTTTTTA 60
AGCCTCTCTC TGGTTTTTCAG TAGAGTTTGA CCTTAAATAT CATCTTTGAT TACTATTGGT 120
GTCCTTGTA TAGGTTTCTT TGCAAAAGTT TGAGTGCAAG TTTTAAGCTA AAAACACGTT 180
TTTAAACTTT CACAAATTTT GTAAGATGAC AATAGCATTC TGTAACATAG ACATTATGGT 240
AATAGTGATT TTCTCTCCAT CCCTATTTTG TCCAGCGATT TCCAAGTTAT AAGACGTGAA 300
TAAGACTAAC CGCTCACTTC CACCAGCAGC TGACCTGGTG GGCTTTTGAG TTCAAAGAGT 360
CATTTCTTCA TCTTACCTCC AGCACTGCAG GGCCGTGTGA CCTTGCAGAG CCTTGTCTCT 420
CATTGATGAA AGGAGCTCAT GCCTCATGAA GCCACTGGTA AGGGCCATGG AGCTCACGGG 480
CCATCAAGCT TCCTTCCCAT CACTTGTGGG TGGGAATTGAC ATTACCCGAT GAGCTCTTCC 540
TGGGGTCACC TGGGAGGGAG TGGCCCATGG GTGGTATGAC AAAATCTCAT AGTCAGTCTT 600
TGCAGTTTTT TCCACAGGTA AAATGAGATT TTGGAATAAT TTCATTGTGT TGTATTTGTC 660
CCAAGGTGAG TCTTACATAT TTTGAGCAAC AAAACGAAGA TCATTATGAA AATGTCCTTA 720
TGGAAGCACT CTAGGGCCAT TGCTCATTTT TATGAGTCCT CGTGCTAAGT CCCTGAGTAC 780
TGTGGCTCAT GTCTTAGCTG GCTAAATCAC AGTCAAAATT CTCTTCTTAA GCCTCAAAAT 840
AAGCTGCTGA TTATACTGCC TGTGGCCAG ACTAATCAAA TACATTTGAT GTTTTAGCTG 900
ACTCCAGATA CTTTTCTTTC CTCCTCCTTG GTTCTTTAAC TGTCATCCCA GATCTGCGAC 960
ATGCAATAAG GAAAAGTGA TCAGGGAGGA AGTAGGATTC CTTTTGCTGC TAGGAACCAC 1020
GTTAGCTTTG GATTGTCCAT AGAATGCACC CTTAACAGTT CTTGGAAAAT GGATGATATT 1080
TGGTTCCTGC CCCATGTTCA GTGTTCTTTG GCAGCTGCAA AGCATATCCT AGCTAGAATC 1140
CTTATCGTCT TGAAGTTCAT CAAAGATTTT GAACAGTCAT GGTGGAGATA CAACCTAAGT 1200
ACATTCATGC CCATTGAGAC AATCCTTTGG TTTGAGCGAC GGAAGGAGGA ATAAACACAT 1260
GAATGTATTT TATTGAATCC CAGAGACCCT GAAACACCAA GACTCATTAA TATATGCATA 1320
CATGGATGGC AGAATAATAA ACCTCACCTG ACCTGTGAGT GTACTCTCAG TTTTAAAGGT 1380
TCTCCCAAAA CAGGGAAACT GAAAAATACT TGGGCAGAAA GAAAAATATCA TCAAATAACA 1440
CCTATTTCTT TTCAGCTATA GAGATGGCTG GATATCAAAA GCACCACGGG AGCTTTGCAA 1500
TTTGCTGCTC TTTTCAGCCC TCAGCTTGAC TCTCAGTTTT CAAGAGGGAG AAAATGAATG 1560
TTTCCCAGCA TTCTCTGTCC TTTGCTCCAA AGAAGAGAGC AGGTGTTGGC TTCCAAACCT 1620
TCCGTATTTT CTTATTGCTG TTAGGGGGAT CAACTGCATG TTTCTGAGG GAAAAGGGTG 1680
GCTCACTGAC CTACTTGAAG GCATTCTCTC AGTGGAAGCT GGGCAAGAGA ATCCAGGGAT 1740
TTCTTTTGCA GGTTTCTGCG CAGTGCCCCT GCCATCAAGC TGCCTAAAT GTGAATATTG 1800
CTTCCCTGCG TTTCAGAGGT GGTAATATTG GGGCAAGTGG TGGAGGATCT AAAAAAAAAA 1865
AAAAA

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(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

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Met Asn Val Ser Gln His Ser Leu Ser Phe Ala Pro Lys Lys Arg Ala
 1             5             10             15
Gly Val Gly Phe Gln Thr Phe Arg Ile Phe Leu Leu Leu Gly Gly
          20             25             30

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Ser Thr Ala Cys Phe Leu Arg Glu Lys Gly Gly Ser Leu Thr Tyr Leu
35 40 45

Lys Ala Phe Ser Gln Trp Lys Leu Gly Lys Arg Ile Gln Gly Phe Leu
50 55 60

Leu Gln Val Ser Ala Gln Cys Pro Cys His Gln Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TATGTATTTG ACAGCATGGT ATAATGAAAA GAGCAGTTGG ACCAGAAGGT AAATTCTAGT 60
CCAGATTTTG ACATTTAGAT GTGTATATAT GGGAAAGTTT CTTAAACTT CGAGTTAATT 120
TTTCTCATCT GTGAAATAAA GGGATTGGAC TAGATACTCT TTAATAGATA TTCCTTATAT 180
GCTTGTCTCC TTCTAGGTCT AAAATTCTGA TCCTTTAGTA GTTTATAAAT GATTATTGGT 240
ATCATTTTCA TCATTTTAGG AGCTCTTTTT TAAAAAATTA TTATTATTTT TTTTGCTCTG 300
TAGCCCATTT CTAGAACATC TTGGGAGTTC TAATTATGTT TTAGATAACA TAAAAAGCAT 360
AGAATCAGAC ATAGTTAAGC AAGAATTTCA CTTAGTTCCC TAGTTTTTAC AGTCTAAATA 420
CATTTTTCTT TCTTTAAAC TGGAGGTTAC TGATACCACC ATTTTCGTCA CCAACAGCCT 480
AATAATTCAC AAAGCTATTT GCTAATTTTT GACACTTTTT TCTTGCCAG TACCATTAAG 540
GGATTTGAAT TTTTTTGAGG TTCCATGTTT ATTTCTTTAG TTATGAGTAT GACCTTGGAC 600
AAGTTACTTC TCTGTACCTG TAAAGTGAGA GTAAAATAAC ATCTAGTTCA TAGGGTTGTT 660
GACTAGTACC TGGCCCATGG TAATCACTGT GTCATGTTGG CTGTTACTAC CCTTTAACAT 720
GATTTGCTCC CCTCCCTGTG GTAAAAAGTA TTCATTGGCA CTACTAATTA ATCTGTTAGC 780
TCAACATATA CTAACCAAAA TGGAAATTTG TTTTGTGAAA TACAATTGTC AGTTCCTTTT 840
CATTATAAGA AACGTTAGTT TATTAGTAGT ATATACCCCT GAGAAAGCAC TAATTTATTT 900
TGAAATTGAG TGGATTAATT CATAATATGA AAGCTGAGAA TGTAGATTGT CTTCTTTCTC 960
TATTTTGAAT AGTTCATAGA ATAATTTATT TCTTTTATCT GGAACAAAA ATAAGTGGTC 1020
TAATTTGTGA CATTCTCAA CATATTTTAC AAGTTTAGAT AAGTTGAGAA TGGCAAAAC 1080
CACAATTACT TTTGCAACAA TCTAATACTT TTAGAAGAAA AATCTATCTT ACCTTATTTT 1140
ATACTAAAAA AAAAAAAAAA GGCCAAAGAG GCCTACAGGA TTTTGAGATG GAGGAACACA 1200
TATTTAATTC CCCTTTATGC CTTGTTCTT GCTCCTCTTT CCACGTTGGA TAACAATTTT 1260
TTGGTTGTTT TGTTTAAAGT GGTGCTCTGA AGCTTAATCT CAGTACCCTT TACTCTGAAT 1320
TGTCAAATTT TGATAAAACG TGCCATTTTC TTTGGTAAGA GAAAGCAGGT CTTAATGTCT 1380
GCCAGAACAC AATTTATATG CCTTATTGGC TTCATTAAAC TTTTAGAAAA CTTTAGCATT 1440
TGTTACTTTT TTCCATTGCA TTTACTTTCA AATGCACCTA ATGAATTCGT CACCCAGTCG 1500
CAACTTTTCC CTTCTCTGTC CCATTGCTTT CTCCTTTCCC CGACGCACAG AATAAACATG 1560
AAGCTCAGCA GTAGAAGCGT AATGATTTCC CTCAGGAAAA ACTTCTGACA GCTAGGTTTT 1620
TCAAGGGTTT CCCTGTGCTA GCTGAGATGC AAAACAAATC ATGGAAGATT GCATACCTGT 1680
TGAGGTATTT AAAACAAGT TGACTTTTTT AGTTTCTTGA ACGGTTAAGG GTGGATTATA 1740
AAAGTAGACA GTTTAGTTT GGGGAACAGA AGCTCTCTTC GTCTTAAGCC AGATTCTCTG 1800
ATTCTTTTAG ACGTCATAGC TCCTTAGTTC TGCTCCTGTC GCCCTAACTT GGCATGGGCA 1860
AGTTGAAGTT CATCCTTAGA CTGCAGCGTT CTGAGCATGG CTGAAGTATT AAAATGTTTA 1920

ATATTTTTTTA GAGCAAAATT GATGGAAAGC ATTTGGCTGA ATCTAAAGAC CTGCAGTCAG 1980
 ATTCTTCAAT GTGGTTTACC CAACTGGAGT AGTGATAAAC ACCTTAATCA TAAAATGAAT 2040
 AAAACAAAA AAACCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 2094

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Ala Arg Thr Gln Phe Ile Cys Leu Ile Gly Phe Ile Lys Leu
 1 5 10 15
 Leu Glu Asn Phe Ser Ile Cys Tyr Phe Phe Pro Leu His Leu Leu Ser
 20 25 30
 Asn Ala Pro Asn Glu Phe Val Thr Gln Ser Gln Leu Phe Pro Ser Leu
 35 40 45
 Ser His Cys Phe Leu Leu Ser Pro Thr His Arg Ile Asn Met Lys Leu
 50 55 60
 Ser Ser Arg Ser Val Met Ile Ser Leu Arg Lys Asn Phe
 65 70 75

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AAATTCAACA TAAACCCAAA TCTGTACTTC TCCAGAGGAG CAGCTCTGAG GTAGAAATTA 60
 CAACGATGAA AAGAGCACAA CGTACAAAAC CAAGAAAGAG TCTGTTGTGT GAAGGGTCAT 120
 TCGATGAAGA AGCTTCTGCA CAGTCCTTTC AGGAAGTGTT AAGTCAATGG AGAACCGGAA 180
 ATCATGATGA CAACAAGAAA CAGAATTTAC ATGCAGCAGT AAAAGACTCA TTGGAAGAAT 240
 GCGAAGTACA GACTAATCTG AAAATTTGGA GAGAACCACT TAATATTGAA CTTAAAGAAG 300
 ACATTCTATC CTATATGGAA AAATTATGGC TTAATAAACA CAGGAGAACT CCACAAGAGC 360
 AACTTTTTTA AATGCTACCA GATACGTTCC CACATCCACA TGAAACCACT GGTGATGCAC 420

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AGTGTTCCTCA  AAATGAAAAC  GATGAAGATA  GTGATGGTGA  GGAGACCAAA  GTACAACACA  480
CAGCTCTTTT  ATTGCCAGTA  GAAACATTAA  ACATAGAGAG  ACCTGAACCA  TCTCTAAAGA  540
TAGTCGAACT  GGATGATACT  TATGAAGAGG  AATTTGAAGA  AGCAGAAAAT  ATTGTGCCTT  600
ACAAAGTTAA  ATTAGCTGAT  GCAGACAGTC  AACGAAGTTG  TGCTTTTCAT  GATTGTCAGA  660
AGAATAGCTT  TCCATATGAA  AATGGCATCC  ATCAACATCA  TGTTTTTCGAT  AAGGGAAAGA  720
GAGACTTCTT  AAATCTTTGT  CTGAGAAACA  GCTATACTTA  TTATAAAGAT  AATTCAAAAG  780
CAGAACTTC  AAACACAGAT  TTTGACAACA  TCGTGGATCC  TGATGTGTAT  TCTTCTGACA  840
TTGAAAAAAT  TGAGGAAAGC  ACCTCCTTTG  AAAGAAATTT  AAAGGAGAAA  AATATAGGTT  900
TAGAAAGTAA  TCAAAAGTCT  GATGATTCCT  GTGTATCACT  TGAAAGCAAG  GACACTTTGC  960
TAGGTAGAGA  TTTAGAAAAA  GCTCCCATTG  AGGAGAAATT  ATCTCAAGAC  ATCAAAGAAT  1020
CCTTGGAATT  GAGCAATCTG  TATAAGAGGC  CAAGCTTTGA  AGAATCAAAA  ACTACAAAGT  1080
CATCACTGTT  GTTACAAGAA  ATAGCCTGCA  GAAGTAAGCC  TATAACAAAA  CAATATCAAG  1140
GACTTGAGAG  ATTCTTTATT  TTTGATACAA  ATGAAAGACT  CAACTTACTT  CCTTCTCATC  1200
GTTTAGAATG  CAACAATTCC  AGTACTAGGA  TTACTATTGC  AGAAGACAGA  GAATGGATTTC  1260
CAGACCATAG  CTTAAGTGAA  TATGCTGATA  ATGCAATTGT  CTTGGGTGTT  CTGCAGGGTG  1320
CTCAGAGTCC  ATCATCAAGT  AGAAAACAGC  AAAAGATGGG  TCAGAAATCA  CAGAGACCTT  1380
CAACAGCAAA  TTTTCCACTT  TCCAACCTCG  TTAAGAAAG  CTCCAGTTGC  CTTTCATCCT  1440
CTCATCCTCG  ATCAAGAAGT  GCAGCTGCTC  AATCATCATC  TAGAGCTGCT  TCTGAAATTT  1500
CAGAAATTGA  ATATATTGAT  ATTACTGACC  AGAATGAGCT  TTCCTTAGAT  GACACTACTG  1560
ATCAACATAC  TTAGACAAT  TTGAAAAAG  AATTACAAGT  GCTGAGATCT  CTTGCAGATA  1620
CTTCAGAAAA  GCTTTACAGC  TTAACCTCAG  AAGAGTTCCC  AGATTTCAGC  AGCCAATCAC  1680
TGAATATAAG  TCAGATTTC  ACAGATTTC  TTAAGACCTC  ACATGTGAGG  GGTCCCTGTG  1740
GAGTTGAGGA  ATTGAGCTGT  TCTGGAAGAG  ATACCAAAAT  TCAGTCTTTG  CTGTCACTTT  1800
CTGAGAGCAG  TACAGATGAG  GAGGAGGAAG  ATTTTCTCAA  CAAGCAACAT  GTCATCACAC  1860
TACCGTGGTC  AAAGAGTACT  TAAAGATTAT  TTGTTTATTA  CTGTTTCCAT  TTTGTACCCA  1920
GAGTAAAGCA  AACAACAGT  AAAAGTAACC  AAGTGATTAC  CTATCCAAGT  GCTGGAGATT  1980
TTGATTACTA  ATGTCTTTGA  TGTTTCAAGG  CTACAAACTA  ATAAAAGTAA  AATTATAAGT  2040
TCAAAAAAAA  AAAAAAAA  AAAAAAAA  2069

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(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Met Lys Arg Ala Gln Arg Thr Lys Pro Arg Lys Ser Leu Leu Cys Glu
 1             5             10             15

Gly Ser Phe Asp Glu Glu Ala Ser Ala Gln Ser Phe Gln Glu Val Leu
      20             25             30

Ser Gln Trp Arg Thr Gly Asn His Asp Asp Asn Lys Lys Gln Asn Leu
      35             40             45

His Ala Ala Val Lys Asp Ser Leu Glu Glu Cys Glu Val Gln Thr Asn
      50             55             60

Leu Lys Ile Trp Arg Glu Pro Leu Asn Ile Glu Leu Lys Glu Asp Ile
      65             70             75             80

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Leu	Ser	Tyr	Met	Glu	Lys	Leu	Trp	Leu	Lys	Lys	His	Arg	Arg	Thr	Pro	
				85					90					95		
Gln	Glu	Gln	Leu	Phe	Lys	Met	Leu	Pro	Asp	Thr	Phe	Pro	His	Pro	His	
			100				105				110					
Glu	Thr	Thr	Gly	Asp	Ala	Gln	Cys	Ser	Gln	Asn	Glu	Asn	Asp	Glu	Asp	
		115				120			125							
Ser	Asp	Gly	Glu	Glu	Thr	Lys	Val	Gln	His	Thr	Ala	Leu	Leu	Leu	Pro	
		130				135				140						
Val	Glu	Thr	Leu	Asn	Ile	Glu	Arg	Pro	Glu	Pro	Ser	Leu	Lys	Ile	Val	
145				150				155							160	
Glu	Leu	Asp	Asp	Thr	Tyr	Glu	Glu	Glu	Phe	Glu	Glu	Ala	Glu	Asn	Ile	
				165				170						175		
Val	Pro	Tyr	Lys	Val	Lys	Leu	Ala	Asp	Ala	Asp	Ser	Gln	Arg	Ser	Cys	
			180				185						190			
Ala	Phe	His	Asp	Cys	Gln	Lys	Asn	Ser	Phe	Pro	Tyr	Glu	Asn	Gly	Ile	
		195				200				205						
His	Gln	His	His	Val	Phe	Asp	Lys	Gly	Lys	Arg	Asp	Phe	Leu	Asn	Leu	
		210				215				220						
Cys	Leu	Arg	Asn	Ser	Tyr	Thr	Tyr	Tyr	Lys	Asp	Asn	Ser	Lys	Ala	Glu	
225				230				235							240	
Thr	Ser	Asn	Thr	Asp	Phe	Asp	Asn	Ile	Val	Asp	Pro	Asp	Val	Tyr	Ser	
			245				250						255			
Ser	Asp	Ile	Glu	Lys	Ile	Glu	Glu	Ser	Thr	Ser	Phe	Glu	Arg	Asn	Leu	
			260				265						270			
Lys	Glu	Lys	Asn	Ile	Gly	Leu	Glu	Ser	Asn	Gln	Lys	Ser	Asp	Asp	Ser	
		275				280				285						
Cys	Val	Ser	Leu	Glu	Ser	Lys	Asp	Thr	Leu	Leu	Gly	Arg	Asp	Leu	Glu	
		290				295				300						
Lys	Ala	Pro	Ile	Glu	Glu	Lys	Leu	Ser	Gln	Asp	Ile	Lys	Glu	Ser	Leu	
305				310				315							320	
Glu	Leu	Ser	Asn	Leu	Tyr	Lys	Arg	Pro	Ser	Phe	Glu	Glu	Ser	Lys	Thr	
			325				330						335			
Thr	Lys	Ser	Ser	Leu	Leu	Leu	Gln	Glu	Ile	Ala	Cys	Arg	Ser	Lys	Pro	
			340				345						350			
Ile	Thr	Lys	Gln	Tyr	Gln	Gly	Leu	Glu	Arg	Phe	Phe	Ile	Phe	Asp	Thr	
		355				360				365						
Asn	Glu	Arg	Leu	Asn	Leu	Leu	Pro	Ser	His	Arg	Leu	Glu	Cys	Asn	Asn	
		370				375				380						

CCCTGGATG

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Ser Ser Thr Arg Ile Thr Leu Ala Glu Asp Arg Glu Trp Ile Pro Asp
385                               390                               395                               400

His Ser Leu Ser Glu Tyr Ala Asp Asn Ala Ile Val Leu Gly Val Leu
                               405                               410                               415

Gln Gly Ala Gln Ser Pro Ser Ser Ser Arg Lys Gln Gln Lys Met Gly
                               420                               425                               430

Gln Lys Ser Gln Arg Pro Ser Thr Ala Asn Phe Pro Leu Ser Asn Ser
                               435                               440                               445

Val Lys Glu Ser Ser Ser Cys Leu Ser Ser Ser His Pro Arg Ser Arg
                               450                               455                               460

Ser Ala Ala Ala Gln Ser Ser Ser Arg Ala Ala Ser Glu Ile Ser Glu
465                               470                               475                               480

Ile Glu Tyr Ile Asp Ile Thr Asp Gln Asn Glu Leu Ser Leu Asp Asp
                               485                               490                               495

Thr Thr Asp Gln His Thr Leu Asp Asn Leu Glu Lys Glu Leu Gln Val
                               500                               505                               510

Leu Arg Ser Leu Ala Asp Thr Ser Glu Lys Leu Tyr Ser Leu Thr Ser
                               515                               520                               525

Glu Glu Phe Pro Asp Phe Ser Ser Gln Ser Leu Asn Ile Ser Gln Ile
                               530                               535                               540

Ser Thr Asp Phe Leu Lys Thr Ser His Val Arg Gly Pro Cys Gly Val
545                               550                               555                               560

Glu Glu Leu Ser Cys Ser Gly Arg Asp Thr Lys Ile Gln Ser Leu Leu
                               565                               570                               575

Ser Leu Ser Glu Ser Ser Thr Asp Glu Glu Glu Glu Asp Phe Leu Asn
                               580                               585                               590

Lys Gln His Val Ile Thr Leu Pro Trp Ser Lys Ser Thr
                               595                               600                               605

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(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCCTGGATG GCGGAGCCTT GGGTTCCGGG GGCCTGGGAC CTGCAACTCT TTCTACAAGA 60



TATCAAGTTA TTCTAGTACA ACCATATAAA TAAATAATAC CTGAAGTCTC AGTGTAACAT 120
GGACAATTAA CAGTGATGAC AGATAAATAC AGACGCATGG GGATCAAATA CTAGGCCAAAA 180
CGCTTTTTTAA AAGTGTATCA GGCTTTTTAAG AAACACTGCA GGATCCTGTC TATCTTAATG 240
CTGATAGAGC TCAGCTAAAA ATTTAGGAGG TTCTAGTATT CTTTATGGCT GAAGCTGAGA 300
GAGTCTGAAA CCCTGATGCT TAAGCTCCAT TCTAGATCAT AGCTCCAACCT CCTTCAGGAT 360
ATAAGGAAAA GAGATTATAT TTCCACAATG ATAGATCTTT GGTGTACAG GTTTCCCAAT 420
GAGTGGATCA TGATGACCGT ATTGTAGGGA CTTGCCATAG TATGGCTGCT TCCCGATCTA 480
CTCGTGTTAC MAGATCAACA GTGGGGTTAA ACGGCTTGGA TGAATCTTTT TGTGGTAGAA 540
CTTTAAGGAA TCGTAGCATT GCGCATCCTG AAGAAATCTC TTCTAATTCT CAAGTACGAT 600
CAAGATCACC AAAGAAGAGA CCAGAGCCTG TGCCAATTCA GAAAGGAAAT AATAATGGGA 660
GAACCACTGA TTTAAACAG CAGAGTACCC GAGAATCATG GGTAAGCCCT AGGAAAAGAG 720
GACTTTCTTC TTCAGAAAAG GATAACATAG AAAGGCAGGC TATAGAAAAT TGTGAGAGAA 780
GGCAAACAGA ACCTGTTTCA CCAGTTTTAA AAAGAATTAA GCGTTGTCTT AGATCTGAAG 840
CACCAAACAG TTCAGAAGAA GATTCTCCTA TAAAATCAGA CAAGGAGTCA GTAGAACAGA 900
GGAGTACAGT AGTGGACAAT GATGCAGATT TTAAGGGAC TAAACGAGCT TGTGATGTC 960
TTTACTGGA TGATTGTGAG AAAAGGGAAA TTAAGGAGGT GAATGTCAGT GAGGAAGGGC 1020
CACTTAATTC TGCAGTAGTT GAAGAAATCA CAGGCTATTT GGCTGTCAAT GGTGTTGATG 1080
ACAGTGATTC AGCTGTTATA AACTGTGATG ACTGTCAGCC TGATGGGAAC ACTAAACAAA 1140
ATAGCATTGG TTCCTATGTG TTACAGGAAA AATCAGTAGC TGAAAATGGG GATACGGATA 1200
CCCAAACCTC AATGTTCCCTT GATAGTAGGA AGGAGGACAG TTATATAGAC CATAAGGTGC 1260
CTTGACACAGA TTCACAAGTG CAGGTCAAGT TGGAGGACCA CAAAATAGTA ACTGCCTGCT 1320
TGCCTGTGGA ACATGTTAAT CAGCTGACTA CTGAGCCAGC TACAGGGCCC TTTTCTGAAA 1380
CTCAGTCATC TTTAAGGGAT TCTGAGGAGG AAGTAGATGT GGTGGGAGAT AGCAGTGCCT 1440
CAAAAGAGCA GTGTAAAGAA AACACCAATA ACGAACTGGA CACAAGTCTT GAGAGTATGC 1500
CAGCCTCCGG AGAACCTGAA CCATCTCCTG TTCTAGACTG TGTATCAGCT CAAATGATGT 1560
CTTTATCAGA ACCTCAAGAA CATCGTTATA CTCTGAGAAC CTCACCACGA AGGGCAGCCC 1620
CTACCAGAGG TAGTCCCCTT AAAACAGTT CTCCTTACAG AGAAAATGGA CAATTTGAGG 1680
AGAATAATCT TAGTCCTAAT GAAACAAATG CAACTGTTAG TGATAATGTA AGTCAATCTC 1740
CTACAAATCC TGGTGAAAT TCTCAAAATG AAAAAGGGAT ATGTTGTGAC TCTCAAAATA 1800
ATGGAAGTGA AGGAGTAAGT AAACCACCCT CAGAGGCAAG ACTCAATATT GGACATTTGC 1860
CATCTGCCAA AGAGAGTGCC AGTCAGCACA TTACAGAAGA GGAAGATGAT GATCCTGATG 1920
TTTATTACTT TGAATCAGAT CATGTGGCAC TGAACACAA CAAAGATTAT CAGAGACTAT 1980
TACAGACGAT TGCTGTACTC GAGGCTCAGC GTTCTCAAGC AGTCCAAGAC CTTGAAAGTT 2040
TAGGCAGGCA CCAGAGAGAA GCACTGAAAA ATCCCATTTG ATTTGTGGAA AAACCTCAGA 2100
AGAAGGCTGA TATTGGGCTT CCATATCCAC AGAGAGTTGT TCAATTGCCT GAGATCGTAT 2160
GGGACCAATA TACCCATAGC CTTGGGAATT TTGAAAGAGA ATTTAAAAAT CGTAAAAGAC 2220
ATACTAGAAG AGTTAAGCTA GTTTTTGATA AAGTAGGTTT ACCTGCTAGA CCAAAAAGTC 2280
CTTTAGATCC TAAGAAGGAT GGAGAGTCCC TTTTATATTC TATGTTGCCT TTGAGTGATG 2340
GTCCAGAAGG CTCAAGCAGT CGTCCTCAGA TGATAAGAGG ACGCTTGTGT GATGATACCA 2400
AACCTGAAAC ATTTAACCAG TTGTGGACTG TTGAAGAACA GAAAAAGCTG GAACAGCTAC 2460
TCATCAATA CCCTCCTGAA GAAGTAGAAT CTCGACGCTG GCAGAAGATA GCAGATGAAT 2520
TGGGCAACAG GACAGCAAAA CAGGTTGCCA GCCGAGTACA GAAGTATTTT ATAAAGCTAA 2580
CTAAAGCTGG CATTCCAGTA CCAGGCAGAA CACCAAACCT ATATATATAC TCCAAAAGT 2640
CTTCAACAAG CAGACGACAG CACCCTCTTA ATAAGCATCT CTTTAAGCCT TCCACTTTCA 2700
TGACTTCACA TGAACCGCCA GTGTATATGG ATGAAGATGA TGACCGATCT TGTTTTTATA 2760
GCCACATGAA CACTGCTGTT GAAGATGCAT CAGATGACGA AAGTATTCCT ATCATGTATA 2820
GGAATTTACC TGAATATAAA GAACTATTAC AGTTTAAAAA GTTAAAGAAG CAGAACTTC 2880
AGCAAATGCA AGCTGAAAGT GGATTTGTGC AACATGTGGG CTTAAGTGT GATAACTGTG 2940
GCATAGAACC CATCCAGGGT GTTCGGTGGC ATTGCCAGGA TTGTCCTCCA GAAATGCTT 3000
TGGATTTCTG TGATTCTTGT TCAGACTGTC TACATGAAAC AGATATTCAC AAGGAAGCAT 3060
ACCAATTAG ACCTATTTAT AGGTCAGGA CATTCTTAGA CAGAGACTAC TGTGTGTCTC 3120
AGGGCACCAG TTACAATTAC CTTGACCCAA ACTACTTTCC AGCAAAACAGA TGACATGGAA 3180
GAGAACATCA TTTACTAGTC CTCTTCAACA CATAGCAATG GTATCATTGT TAATTATGTG 3240
CACAGTTTGG AAAGATTCTC TGCTTTCCCA GAAATGACAC TCACAGCATG AGAGCTTCCT 3300

GAGTGTTCCTC GTCAAGTACA GCTCTGCACC GTTGTGGCTC TAGATCACTG TTCAGCAGCT 3360
 GAACATTCCCT GGTGAGCAAA GGTTTCCCTG GTGAATTTTT CACCACTGCG TTTTAGGTGG 3420
 TGATCTTAAA TGGGTGAGAT GGAACGAGAG CACACATTAA AGAGAGAGTA AATTCCAAAG 3480
 GTTTCAAAGA ACTTGGTCAT AAATATGATA ATGAGAAGAC AAAGTATTTA TATTAAAACA 3540
 GTTTAGTAGC CTTCAGTTTT GTGAAAATAG TTTTCAGCAC AGAAACTGAC TTCTTTAGAC 3600
 AAAGTTTTAA CCAATGATGG TGTGTGCTTC TAGGATATAC ACTTTAAAAG AACTCACTGT 3660
 CCCAGTGGTG GTCATTGATG GCCTTTAGTA AATTGGAGCT GCTTAATCAT ATTGATATCT 3720
 AATTTCTTTT AACCACAATG AATTGTCCTT AATTACCAAC AGTGAAGCAC TACAGGAGGC 3780
 AACTGTGGCA TTGCTTCCTT AACCAGCTCA TGGTGTGTGA ATGTTATAAA ATTGTCACCTC 3840
 AGATATATTT TTTAAATGTA ATGTTATATA AGATGATCAT GTGATGTGTA CAACTATGG 3900
 TGAAAAGTGC CAGTGGTAGT AACTGTGTAA AGTTTCTAAT TCACAACATT AATTCCTTTA 3960
 AAATACACAG CTTTCTGCCT CTGTATTTGG AGTTGTCACT ACAACTCATC AAAGAAAAC 4020
 GCCTAATATA AAAATCATAT ATATGGTAAT AATTTCCCTC TTTTGTAGTC TGCACAAGAT 4080
 CCATAAAGA TTGTATTTTT ATTACTATTT AAACAAGTGA TTAAATTTAG TCTGCACAGT 4140

 GAGCAAGGGT TCACATGCAT TCTTTTATAC TGCTGGATTT TGTTGTGCAT CATTTAAAAC 4200
 ATTTTGTATG TTTCTTCTTA TCTGTGTATA CAGTATGTTT TTGAATGATG TTCATTTGTC 4260
 AGGAGAACTG TGAGAAATAA ACTATGTGGA TACTGTCTGT TTMTRTCAAA AAAAAAAAAA 4320
 AAAAAAAAAA AAAAAA 4337

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Ala Ala Ser Arg Ser Thr Arg Val Thr Arg Ser Thr Val Gly Leu
 1 5 10 15
 Asn Gly Leu Asp Glu Ser Phe Cys Gly Arg Thr Leu Arg Asn Arg Ser
 20 25 30
 Ile Ala His Pro Glu Glu Ile Ser Ser Asn Ser Gln Val Arg Ser Arg
 35 40 45
 Ser Pro Lys Lys Arg Pro Glu Pro Val Pro Ile Gln Lys Gly Asn Asn
 50 55 60
 Asn Gly Arg Thr Thr Asp Leu Lys Gln Gln Ser Thr Arg Glu Ser Trp
 65 70 75 80
 Val Ser Pro Arg Lys Arg Gly Leu Ser Ser Ser Glu Lys Asp Asn Ile
 85 90 95
 Glu Arg Gln Ala Ile Glu Asn Cys Glu Arg Arg Gln Thr Glu Pro Val
 100 105 110
 Ser Pro Val Leu Lys Arg Ile Lys Arg Cys Leu Arg Ser Glu Ala Pro
 115 120 125

Asn	Ser	Ser	Glu	Glu	Asp	Ser	Pro	Ile	Lys	Ser	Asp	Lys	Glu	Ser	Val
130						135				140					
Glu	Gln	Arg	Ser	Thr	Val	Val	Asp	Asn	Asp	Ala	Asp	Phe	Gln	Gly	Thr
145					150					155					160
Lys	Arg	Ala	Cys	Arg	Cys	Leu	Ile	Leu	Asp	Asp	Cys	Glu	Lys	Arg	Glu
				165					170					175	
Ile	Lys	Lys	Val	Asn	Val	Ser	Glu	Glu	Gly	Pro	Leu	Asn	Ser	Ala	Val
			180					185					190		
Val	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Ala	Val	Asn	Gly	Val	Asp	Asp	Ser
		195					200					205			
Asp	Ser	Ala	Val	Ile	Asn	Cys	Asp	Asp	Cys	Gln	Pro	Asp	Gly	Asn	Thr
	210					215					220				
Lys	Gln	Asn	Ser	Ile	Gly	Ser	Tyr	Val	Leu	Gln	Glu	Lys	Ser	Val	Ala
225					230					235					240
Glu	Asn	Gly	Asp	Thr	Asp	Thr	Gln	Thr	Ser	Met	Phe	Leu	Asp	Ser	Arg
				245					250					255	
Lys	Glu	Asp	Ser	Tyr	Ile	Asp	His	Lys	Val	Pro	Cys	Thr	Asp	Ser	Gln
			260					265					270		
Val	Gln	Val	Lys	Leu	Glu	Asp	His	Lys	Ile	Val	Thr	Ala	Cys	Leu	Pro
		275					280					285			
Val	Glu	His	Val	Asn	Gln	Leu	Thr	Thr	Glu	Pro	Ala	Thr	Gly	Pro	Phe
	290					295					300				
Ser	Glu	Thr	Gln	Ser	Ser	Leu	Arg	Asp	Ser	Glu	Glu	Glu	Val	Asp	Val
305					310					315					320
Val	Gly	Asp	Ser	Ser	Ala	Ser	Lys	Glu	Gln	Cys	Lys	Glu	Asn	Thr	Asn
				325					330					335	
Asn	Glu	Leu	Asp	Thr	Ser	Leu	Glu	Ser	Met	Pro	Ala	Ser	Gly	Glu	Pro
			340					345					350		
Glu	Pro	Ser	Pro	Val	Leu	Asp	Cys	Val	Ser	Ala	Gln	Met	Met	Ser	Leu
		355				360						365			
Ser	Glu	Pro	Gln	Glu	His	Arg	Tyr	Thr	Leu	Arg	Thr	Ser	Pro	Arg	Arg
	370					375					380				
Ala	Ala	Pro	Thr	Arg	Gly	Ser	Pro	Thr	Lys	Asn	Ser	Ser	Pro	Tyr	Arg
385					390					395					400
Glu	Asn	Gly	Gln	Phe	Glu	Glu	Asn	Asn	Leu	Ser	Pro	Asn	Glu	Thr	Asn
				405					410					415	
Ala	Thr	Val	Ser	Asp	Asn	Val	Ser	Gln	Ser	Pro	Thr	Asn	Pro	Gly	Glu
			420					425					430		

Ile	Ser	Gln	Asn	Glu	Lys	Gly	Ile	Cys	Cys	Asp	Ser	Gln	Asn	Asn	Gly	435	440	445	
Ser	Glu	Gly	Val	Ser	Lys	Pro	Pro	Ser	Glu	Ala	Arg	Leu	Asn	Ile	Gly	450	455	460	
His	Leu	Pro	Ser	Ala	Lys	Glu	Ser	Ala	Ser	Gln	His	Ile	Thr	Glu	Glu	465	470	475	480
Glu	Asp	Asp	Asp	Pro	Asp	Val	Tyr	Tyr	Phe	Glu	Ser	Asp	His	Val	Ala	485	490	495	
Leu	Lys	His	Asn	Lys	Asp	Tyr	Gln	Arg	Leu	Leu	Gln	Thr	Ile	Ala	Val	500	505	510	
Leu	Glu	Ala	Gln	Arg	Ser	Gln	Ala	Val	Gln	Asp	Leu	Glu	Ser	Leu	Gly	515	520	525	
Arg	His	Gln	Arg	Glu	Ala	Leu	Lys	Asn	Pro	Ile	Gly	Phe	Val	Glu	Lys	530	535	540	
Leu	Gln	Lys	Lys	Ala	Asp	Ile	Gly	Leu	Pro	Tyr	Pro	Gln	Arg	Val	Val	545	550	555	560
Gln	Leu	Pro	Glu	Ile	Val	Trp	Asp	Gln	Tyr	Thr	His	Ser	Leu	Gly	Asn	565	570	575	
Phe	Glu	Arg	Glu	Phe	Lys	Asn	Arg	Lys	Arg	His	Thr	Arg	Arg	Val	Lys	580	585	590	
Leu	Val	Phe	Asp	Lys	Val	Gly	Leu	Pro	Ala	Arg	Pro	Lys	Ser	Pro	Leu	595	600	605	
Asp	Pro	Lys	Lys	Asp	Gly	Glu	Ser	Leu	Ser	Tyr	Ser	Met	Leu	Pro	Leu	610	615	620	
Ser	Asp	Gly	Pro	Glu	Gly	Ser	Ser	Ser	Arg	Pro	Gln	Met	Ile	Arg	Gly	625	630	635	640
Arg	Leu	Cys	Asp	Asp	Thr	Lys	Pro	Glu	Thr	Phe	Asn	Gln	Leu	Trp	Thr	645	650	655	
Val	Glu	Glu	Gln	Lys	Lys	Leu	Glu	Gln	Leu	Leu	Ile	Lys	Tyr	Pro	Pro	660	665	670	
Glu	Glu	Val	Glu	Ser	Arg	Arg	Trp	Gln	Lys	Ile	Ala	Asp	Glu	Leu	Gly	675	680	685	
Asn	Arg	Thr	Ala	Lys	Gln	Val	Ala	Ser	Arg	Val	Gln	Lys	Tyr	Phe	Ile	690	695	700	
Lys	Leu	Thr	Lys	Ala	Gly	Ile	Pro	Val	Pro	Gly	Arg	Thr	Pro	Asn	Leu	705	710	715	720
Tyr	Ile	Tyr	Ser	Lys	Lys	Ser	Ser	Thr	Ser	Arg	Arg	Gln	His	Pro	Leu	725	730	735	

Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser His Glu Pro
740 745 750

Pro Val Tyr Met Asp Glu Asp Asp Arg Ser Cys Phe His Ser His
755 760 765

Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser Ile Pro Ile
770 775 780

Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln Phe Lys Lys
785 790 795 800

Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser Gly Phe Val
805 810 815

Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu Pro Ile Gln
820 825 830

Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met Ser Leu Asp
835 840 845

Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp Ile His Lys
850 855 860

Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr Phe Leu Asp
865 870 875 880

Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr Leu Asp Pro
885 890 895

Asn Tyr Phe Pro Ala Asn Arg
900

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AATCGGGACC CCATCCCCCA AATCACTGGA TCCTGCAGCC CCACATCCTA AGGTGGATCC 60

CACGCTTCCC TGTGCCCCCT ACTGGATCCT GGACCTCTAC GTCTTAACCA CTGGATCCCCA 120

CACAAATCAG TGAATGGATC CCAACACCCC AACCACAGGA GCACGGATTC CCTGTACCTC 180

AACACCCAGA CCCTGCCTCC CTCAGGCACC AGATCCAGTG TCCTAGTGAA ACGCTGGATC 240

CTAGATCCCC AACCCAGAT CCCCATGCCT CGAGCCCTGG ATCTCCAAGC TCAGCTGCTG 300

GATTCTGGAT GTCAACAAAC CTCACCACTG GATCCTGACA ACCACAATGC CTGGATCCTG 360

GGGCCCCCAT CACTGGATCC CAGATCCCCT CACTCCACCC ACTGGATTCC TGCATTGGTT 420

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TTTGGTTTTT TGTTTTTTTT TTAACCTCGA CACTGGGTCT CAGATCCTTC TGCTGACTGC 480
CAGATCCCTG CATTTCAAGC ACTACGCCTT CCACCCCAG GCCTGGATC CCAGATTCCC 540
AAGCCTTCAC CCACCAGATT CTGGCTCCTA AAACAAGTGC GGGGGCCCCA GTGGCACAGC 600
AAGTGGATCC TGGCAACTGC AGCTGCTGGA TTCCAGATTC TGGGTCCCCA ATCCCTCTGC 660
CCAGTCCCTC AATGTTGAAA CCTCATCTCT TGAAGGCAGA TCCTGATATT CCAAGGCACT 720
GAATCCCAAG CCCTGAATCC CCGGTTTCTG ATCTGAATCT TCCAGGCGCC GGGTCCCAA 780
TGTTTCAGGCC CCAAGTCTAG ATCCTGGCAG CCCAGTCACA GAGTATCCCA CACACACTGG 840
TGCCCAGAGC CGGCTTCTCA TGACATGAAA TTGCATGGTC GAGGGAGTCT GTGGGGAAGG 900
AAGCCCAGGT CCTGGCTGCA ACCTGCACGG ATGCTGGATT CCCCCTCACC CCACCTCTGC 960
ATGGCCACCC CCTCCCAGCC CTGTGGGGAA ACTGTTCCCT GGAACCACTC CACTCCCTGC 1020
ATCCCCACAC TTCACAGCAT CTTCATCCC CCTCCCCTT CTAGGCGAAT AGTCCCCAGA 1080
GCTGTGTTCC TCCAAGGGGT CCGAGGAATC ACTCACTCCT GGAGGCTGGC AAGGAGACAG 1140
TCTGAGGCCA GGGACACATG AAGGGATGTC CCCACCCCAG CACTATCAGG GCCTCCCCAG 1200
GCTTCCAGAG TTGAAAGCCA GGAGAAAATC GGCAAAGACC ACCCTTCCCT AAACCCAAGC 1260
ACCCAATGAT GCRAAAAAAA AAAAAAAAAA AAAAAAAAAA 1299

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Met Lys Leu His Gly Arg Gly Ser Leu Trp Gly Arg Lys Pro Arg Ser
 1             5             10             15

Trp Leu Gln Pro Ala Arg Met Leu Asp Ser Pro Ser Pro His Leu Cys
          20             25             30

Met Ala Thr Pro Ser Gln Pro Cys Gly Glu Thr Val Pro Trp Asn His
          35             40             45

Ser Thr Pro Cys Ile Pro Thr Leu His Ser Ile Phe His Pro Pro Pro
          50             55             60

Thr Ser Arg Arg Ile Val Pro Arg Ala Val Phe Leu Gln Gly Val Arg
          65             70             75             80

Gly Ile Thr His Ser Trp Arg Leu Ala Arg Arg Gln Ser Glu Ala Arg
          85             90             95

Asp Thr

```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

CTCCTCTGTC CACTGCTTTC GTGAAGACAA GATGAAGTTC ACAATTGTCT TTGCTGGACT 60
TCTTGAGATC TTTCTAGCTC CTGCCCTAGC TAACTATAAT ATCAACGTCA ATGATGACAA 120
CAACAATGCT GGAAGTGGGC AGCAGTCAGT GAGTGTCAAC AATGAACACA ATGTGGCCAA 180
TGTTGACAAT AACAACGGAT GGGACTCCTG GAATTCCATC TGGGATTATG GAAATGGCTT 240
TGCTGCAACC AGACTCTTTC AAAAGAAGAC ATGCATTGTG CACAAAATGA ACAAGGAAGT 300
CATGCCCTCC ATTCAATCCC TTGATGCACT GGTCAAGGAA AAGAAGCTTC AGGGTAAGGG 360
ACCAGGAGGA CCACCTCCCA AGGGCCTGAT GTACTCAGTC AACCCAAACA AAGTCGATGA 420
CCTGAGCAAG TTCGGAAGAA ACATTGCAAA CATGTGTCGT GGGATTCCAA CACATATGGC 480
TGAGGAGATG CAAGAGGCAA GCCTGTTTTT TTACTCAGGA ACGTGCTACA CGACCAAGTGT 540
ACTATGGATT GTGGACATTT CCTTCTGTGG AGACACGGTG GAGAACTAAA CAATTTTTTA 600
AAGCCACTAT GGATTTAGTC ATCTGAATAT GCTGTGCAGA AAAAATATGG GCTCCAGTGG 660
TTTTTACCAT GTCATTCTGA AATTTTTCTC TACTAGTTAT GTTTGATTTC TTTAAGTTTC 720
ATAAAATCA TTCAGCCTTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780
AAAAAAAAAA A                                     791

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(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu Ala
 1             5             10             15
Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn Asn Asn
      20             25             30
Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu His Asn Val
      35             40             45
Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp Asn Ser Ile Trp
      50             55             60
Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu Phe Gln Lys Lys Thr
      65             70             75             80
Cys Ile Val His Lys Met Asn Lys Glu Val Met Pro Ser Ile Gln Ser
      85             90             95
Leu Asp Ala Leu Val Lys Glu Lys Lys Leu Gln Gly Lys Gly Pro Gly
      100            105            110

```


Gly Pro Pro Pro Lys Gly Leu Met Tyr Ser Val Asn Pro Asn Lys Val
115 120 125

Asp Asp Leu Ser Lys Phe Gly Lys Asn Ile Ala Asn Met Cys Arg Gly
130 135 140

Ile Pro Thr Tyr Met Ala Glu Glu Met Gln Glu Ala Ser Leu Phe Phe
145 150 155 160

Tyr Ser Gly Thr Cys Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile
165 170 175

Ser Phe Cys Gly Asp Thr Val Glu Asn
180 185

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTCAAGTTCA TCATTGTCCT GAGAGAGAGG AGCAGCGCGG TTCTCGGCCG GGACAGCAGA 60
ACGCCAGGGG ACCCTCACCT GGGCGCGCCG GGGCACGGGC TTTGATTGTC CTGGGGTTCGC 120
GGAGACCCGC GCGCCTGCCG TGCACGCCGG GCGGCAACCT TTGCAGTCGC GTTGGCTGCT 180
GCGATCGGCC GCGGGGTCCC TGCCGAAGGC TCGGCTGCTT CTGTCCACCT CTTACACTTC 240
TTCATTTATC GGTGGATCAT TTCGAGAGTC CGTCTTGTA ATGTTTGGA CTTTGCTACT 300
TTATTGCTT TTTCTGGCGA CAGTTCAGC ACTCGCCGAG ACCGGCGGAG AAAGGCAGCT 360
GAGCCCGGAG AAGAGCGAAA TATGGGGACC CGGGCTAAAA GCAGACGTCG TCCTTCCCGC 420
CCGCTATTTT TATATTCAGG CAGTGGATAC ATCAGGGAAT AAATTCACAT CTTCTCCAGG 480
CGAAAAGGTC TTCCAGGTGA AAGTCTCAGC ACCAGAGGAG CAATTCACTA GAGTTGGAGT 540
CCAGGTTTTA GACCGAAAAA ATGGGTCCTT CATAGTAAGA TACAGAATGT ATGCAAGCTA 600
CAAAAATCTG AAGGTGGAAA TTAAATTCCA AGGGCAACAT GTGGCCAAAT CCCCATATAT 660
TTTAAAAGGG CCGGTTTACC ATGAGAAGTG TGAAGTCTCT CTGCAAGATA GTGCAGCCTG 720
GCTACGGGAG ATGAACTGCC CTGAAACCAT TGCTCAGATT CAGAGAGATC TGGCACATTT 780
CCCTGCTGTG GATCCAGAAA AGATTGCAGT AGAAATCCCA AAAAGATTTG GACAGAGGCA 840
GAGCCTATGT CACTACACCT TAAAGGATAA CAAGGTTTAT ATCAAGACTC ATGGTGAACA 900
TGTAGGTTTT AGAATTTTCA TGGATGCCAT ACTACTTTCT TTGACTAGAA AGGTGAAGAT 960
GCCAGATGTG GAGCTCTTTG TTAATTTGGG AGACTGGCCT TTGGAAAAAA AGAAATCCAA 1020
TTCAAACATC CATCCGATCT TTTCCTGGTG TGGCTCCACA GATTCCAAGG ATATCGTGAT 1080
GCCTACGTAC GATTTGACTG ATTCTGTTCT GGAAACCATG GGCCGGGTAA GTCTGGATAT 1140
GATGTCCGTG CAAGCTAACA CGGGTCCTCC CTGGGAAAGC AAAAATTCCA CTGCCGTCTG 1200
GAGAGGGCGA GACAGCCGCA AAGAGAGACT CGAGCTGGTT AAACAGGATG AAAACCTGTA 1260
AGAACTCATA GACGCTGCTT TCACCAACTT TTTCTTCTTT AAACAGGATG AAAACCTGTA 1320
TGGTCCCATT GTGAAACATA TTTCATTTTT TGATTTCTTC AAGCATAAGT ATCAAATAAA 1380
TATCGATGGC ACTGTAGCAG CTTATCGCCT GCCATATTTG CTAGTTGGTG ACAGTGTGTT 1440
GCTGAAGCAG GATTCCATCT ACTATGAACA TTTTACAAAT GAGCTGCAGC CCTGGAAAAC 1500
CTACATTCCA GTTAAGAGCA ACCTGAGCGA TCTGTAGAAA AAACCTAAAT GGGCGAAAGA 1560
TCACGATGAA GAGGCCAAAA AGATAGCAAA AGCAGGACAA GAATTTGCAA GAAATAATCT 1620
CATGGGCGAT GACATATTCT GTTATTATTT CAAACTYTTC CAGGAATATG CCAATTTACA 1680

AGTGAGTGAG CCCCAAATCC GAGAGGGCAT GAMAAGGGTA GAACCACAGA CTGAGGACGA 1740
 CCTCTTCCST TGTACTTGCC ATAGGAAAAA GACCAAAGAT GAACTSTGAT ATGCAAAATA 1800
 ACTTCTATTA GAATAATGGT GCTCTGAAGA CTCTTCTTAA CTAAAAAGAA GAATTTTTTTT 1860
 AAGTATTAAT TCCATGGACA ATATAAAATC TGTGTGATTG TTTGCAGTAT GAAGACACAT 1920
 TTCTACTTAT GCAGTATTCT CATGACTGTA CTTTAAAGTA CATTTTTagA ATTTTATAAT 1980
 AAAACCACCT TTATTTTAAA AAAAAAAAAA AA 2012

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Phe Gly Thr Leu Leu Leu Tyr Cys Phe Phe Leu Ala Thr Val Pro
 1 5 10 15
 Ala Leu Ala Glu Thr Gly Gly Glu Arg Gln Leu Ser Pro Glu Lys Ser
 20 25 30
 Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu Pro Ala Arg
 35 40 45
 Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn Lys Phe Thr Ser
 50 55 60
 Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val Ser Ala Pro Glu Glu
 65 70 75 80
 Gln Phe Thr Arg Val Gly Val Gln Val Leu Asp Arg Lys Asp Gly Ser
 85 90 95
 Phe Ile Val Arg Tyr Arg Met Tyr Ala Ser Tyr Lys Asn Leu Lys Val
 100 105 110
 Glu Ile Lys Phe Gln Gly Gln His Val Ala Lys Ser Pro Tyr Ile Leu
 115 120 125
 Lys Gly Pro Val Tyr His Glu Asn Cys Asp Cys Pro Leu Gln Asp Ser
 130 135 140
 Ala Ala Trp Leu Arg Glu Met Asn Cys Pro Glu Thr Ile Ala Gln Ile
 145 150 155 160
 Gln Arg Asp Leu Ala His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala
 165 170 175
 Val Glu Ile Pro Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr
 180 185 190
 Thr Leu Lys Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val

195	200	205
Gly Phe Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys		
210	215	220
Val Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro		
225	230	235 240
Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp		
	245	250 255
Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu		
	260	265 270
Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu Asp Met Met		
	275	280 285
Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr		
	290	295 300
Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val		
305	310	315 320
Lys Leu Ser Arg Lys His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn		
	325	330 335
Phe Phe Phe Phe Lys Gln Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys		
	340	345 350
His Ile Ser Phe Phe Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile		
	355	360 365
Asp Gly Thr Val Ala Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp		
	370	375 380
Ser Val Val Leu Lys Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn		
385	390	395 400
Glu Leu Gln Pro Trp Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser		
	405	410 415
Asp Leu Leu Glu Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala		
	420	425 430
Lys Lys Ile Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met		
	435	440 445
Gly Asp Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala		
	450	455 460
Asn Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Xaa Arg Val		
465	470	475 480
Glu Pro Gln Thr Glu Asp Asp Leu Phe Xaa Cys Thr Cys His Arg Lys		
	485	490 495
Lys Thr Lys Asp Glu Leu		

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GNAAGAAGAG AGCAACAGCC AGGACCAAG

29

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CNCAGGCTAG GCACTGATTC TGCTGGTTC

29

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GNAGACATGA AAGTTGAGCA GAAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GNGGTGCTTT TGATATCCAG CCATCTCTA

29

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNTGGAAAGA GGAGCAAGAA CCAAGGCAG

29

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TNGGTTTTGT ACGTTGTGCT CTTTTCATC

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATGGTCTA TATAACTGTC CTCCTTCCT

29

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNACACTGGG TCTCAGATCC TTCTGCTGA

29

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GNCTCCAAGA AGTCCAGCAA AGACAATTG

29

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ANTGCCAAAC ATTTACAAGA CGGACTCTC

29

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AGCTCACAGT AGCCCCGGCGG CCCAGGGCAA TCCGACCACA TTCACTCTC ACCGCTGTAG 60

GAATCCAGAT GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA 120
 CCACCATGAG CCTGCATTCT CAAGCCTCTG CCACAACCTCG GCATCCAGAG CCCC GGCGCA 180
 CAGAGCACAG GGCTCCCTCT TCAACGTGGC GACCAGTGGC CCTGACCCTG CTGACTTTGT 240
 GCTTGGTGCT GCTGATAGGG CTGGCAGCCC TGGGGCTTTT GTTTTTTCAG TACTACCAGC 300
 TCTCCAATAC TGGTCAAGAC ACCATTTCTC AAATGGAAGA AAGATTAGGA AATACGTCCC 360
 AAGAGTTGCA ATCTCTTCAA GTCCAGAATA TAAAGCTTGC AGGAAGTCTG CAGCATGTGG 420
 CTGAAAAACT CTGTCTGTGAG CTGTATAACA AAGCTGGAGC ACACAGGTGC AGCCCTTGTA 480
 CAGAACAATG GAAATGGCAT GGAGACAATT GCTACCAGTT CTATAAAGAC AGCAAAAGTT 540
 GGGAGGACTG TAAATATTTT TGCCTTAGTG AAAACTCTAC CATGCTGAAG ATAAACAAAC 600
 AAGAAGACCT GGAATTTGCC GCGTCTCAGA GCTACTCTGA GTTTTCTAC TCTTATTGGA 660
 CAGGGCTTTT GCGCCCTGAC AGTGGCAAGG CCTGGCTGTG GATGGATGGA ACCCCTTTCA 720
 CTTCTGAAC TTTCCATATT ATAATAGATG TCACCAGCCC AAGAAGCAGA GACTGTGTGG 780
 CCATCCTTAA TGGGATGATC TTCTCAAAGG ACTGCAAAGA ATTGAAGCGT TGTGTCTGTG 840
 AGAGAAGGGC AGGAATGGTG AAGCCAGAGA GCCTCCATGT CCCCCCTGAA ACATTAGGCG 900
 AAGGTGACTG ATTCGCCCTC TGCAACTACA AATAGCAGAG TGAGCCAGGC GGTGCCAAAG 960
 CAAGGGCTAG TTGAGACATT GGGAAATGGA ACATAATCAG GAAAGACTAT CTCTCTGACT 1020
 AGTACAAAAT GGGTTCTCGT GTTTCCTGTT CAGGATCACC AGCATTTCTG AGCTTGGGTT 1080
 TATGCACGTA TTTAACAGTC ACAAGAAGTC TTATTTACAT GCCACCAACC AACCTCAGAA 1140
 ACCCATAATG TCATCTGCCT TCTTGGCTTA GAGATAACTT TTAGCTCTCT TTCTTCTCAA 1200
 TGTCTAATAT CACCTCCCTG TTTTCATGTC TTCTTTACAC TTGGTGGAAT AAGAAACTTT 1260
 TTGAAGTAGA GGAATACAT TGAGGTAACA TCCTTTTCTC TGACAGTCAA GTAGTCCATC 1320
 AGAAATTGGC AGTCACTTCC CAGATTGTAC CAGCAAATAC ACAAGGAATT CTTTTTGTTT 1380
 GTTTCAGTTC ATACTAGTCC CTTCCTCAATC CATCAGTAAA GACCCCATCT GCCTTGTTCA 1440
 TGCCGTTTCC CAACAGGGAT GTCACTTGAT ATGAGAATCT CAAATCTCAA TGCCTTATAA 1500
 GCATTCTTCC CTGTGTCCAT TAAGACTCTG ATAATTGTCT CCCCTCCATA GGAATTTCTC 1560
 CCAGGAAAGA AATATATCCC CATCTCCGTT TCATATCAGA ACTACCGTCC CCGATATTCC 1620
 CTTCAGAGAG ATTAAAGACC AGAAAAAAGT GAGCCTCTTC ATCTGCACCT GTAATAGTTT 1680
 CAGTTCTTAT TTTCTTCCAT TGACCCATAT TTATACCTTT CAGGTACTGA AGATTTAATA 1740
 ATAATAAATG TAAATACTGT GAAAAAATAA AAAAAA 1776

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
 1 5 10 15
 Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
 20 25 30
 Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
 35 40 45
 Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
 50 55 60
 Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn

65		70		75		80
Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr						
	85			90		95
Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly						
	100		105			110
Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys						
	115		120			125
Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His						
	130		135			140
Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp						
	145		150		155	160
Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn						
	165		170			175
Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe						
	180		185			190
Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala						
	195		200			205
Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile						
	210		215			220
Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu						
	225		230		235	240
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val						
	245		250			255
Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro						
	260		265			270
Pro Glu Thr Leu Gly Glu Gly Asp						
	275		280			

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CAACTATCCC ATAATTTATT TATTCTTCTT CAATGTTTGT AAAGTGCATG AGTCATGTTC 60

ACACTTGAAG TCTAGTAGTG CACTGTAATA ATTCATTTTT TAAAAGATTA TTTAATGCCC 120
 ATTTCAAAAT ACAGTAGTTT ACACAGCTAC AGAAACAATT TGGGGCAAGT TTTAAAACAC 180
 TGAAACAGTA ATAGTTATTG GTGTCACATA AAAGTGATTT GTTTTTTACA GCCAAACCTC 240
 TGTCAGTCAG AGGCATTCAT TAGTTTTATA CATGTAATTT GAAAATCACT AAACCTCGTT 300
 TTCTCAGCAG CAATAATTTA AGAGGCTTCA AAAATATAAT TTCACTCTTA TTTAGTATTT 360
 TTTCTGGGG GGATTTTAC GTAATTTTTT TATGAAAAGA CAAATGCATG TTGAGATAAC 420
 TTCTGGGATT AAAATAGTCT TTTGCTTTAC TTTTTTGGTT TCCTAAAACA ACTTTATTGA 480
 CTTTTAGTCC ATACTGTTAT ATTTTGTCT TAAAGAAAAT TTAACTACA AATACCAAAA 540
 GAAAACATTT TAAATTTAGG GATGAGACTT TGGTGTATCG TGGGTCTAGG TTTAATGAAC 600
 ACATCTGGGG TTAAGTTGGC ATTTCTTCAC ATCTCCACAC CCACACCAAC CATCACAGCC 660
 CCCACCAAC CTTCTCCCA CCCCAAAAGC ATTGTCCAGG GATATAGATT TTACCAAAGG 720
 CTTCTGGGA AGACGAGGGA GCAACACTTT AGATTAAATG TGATCAGACT TTCCTATTAG 780
 ATATGGCTCT TCTGTCTCTT GTTATCCCC TGACAGCTCT GCCATAAAGT CCCTTCTCCT 840
 CATCCTTCCC AAACAGGCTG TATAAGTGCT TTGAGGTAAT TAACTCTTT CCTCCAGTTT 900
 ACAAATATCA CTTAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 947

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Arg Leu Trp Cys Ile Val Gly Leu Gly Leu Met Asn Thr Ser Gly
 1 5 10 15
 Val Lys Leu Ala Phe Leu His Ile Ser Thr Pro Thr Pro Thr Ile Thr
 20 25 30
 Ala Pro His Gln Pro Ser Pro Asn Pro Lys Ser Ile Val Gln Gly Tyr
 35 40 45
 Arg Phe Tyr Gln Arg Leu Pro Gly Lys Thr Arg Glu Gln His Phe Arg
 50 55 60
 Leu Asn Val Ile Arg Leu Ser Tyr
 65 70

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CGCTGACTTG GGCAATGGGG CCGGTGGGGT TTGGGGGCGG AAGAGACCCT CGGGGTTGAG 60

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AAGTATGTGG TGGCCTTTCG TCCCCTGTAA AACATTGTCA CACGGTGTGG GGCGGCAGCG 120
CTGGATCTTT GCAAGGCTAT TTTGGCATTG TGCTGGATAT ATGTTTCGTAA ATACCAAAGT 180
CGGCGGGAAA GTGAAGTTGT CTCCACCATA ACAGCAATTT TTTCTCTAGC AATTGCACTT 240
ATCACATCAG CACTTCTACC AGTGGATATA TTTTGTGGTTT CTTACATGAA AAATCAAAAT 300
GGTACATTTA AGGACTGGGC TAATGCTAAT GTCAGCAGAC AGATTGAGGA CACTGTATTA 360
TACGGTTACT ATACTTTATA TTCTGTTATA TTGTTCTGTG TGTTCCTCTG GATCCCTTTT 420
GTCTACTTCT ATTATGAAGA AAAGGATGAT GATGATACTA GTAAATGTAC TCAAATTAATA 480
ACGGCACTCA AGTATACTTT GGGATTTGTT GTGATTTGTG CACTGCTTCT TTTAGTTGGT 540
GCCTTTGTTC CATTGAATGT TCCCAATAAC AAAAATTCTA CAGAGTGGGA AAAAGTGAAG 600
TCCCTATTTG AAGAACTTGG AAGTAGTCAT GGTTTAGCTG CATTGTCATT TTCTATCAGT 660
TCTCTGACCT TGATTGGAAT GTTGGCAGCT ATAACCTTACA CAGCCTATGG CATGTCTGCG 720
TTACCTTTAA ATCTGATAAA AGGCACTAGA AGCGCTGCTT ATGAACGTTT GGAAAACACT 780
GAAGACATTG AAGAAGTAGA ACAACACATT CAAACGATTA AATCAAAAAG CAAAGATGGT 840
CGACCTTTGC CAGCAAGGGA TAAACGCGCC TTAACAACAAT TTGAAGAAAG GTTACGAACA 900
CTTAAGAAGA GAGAGAGGCA TTTAGAATTC ATTGAAAACA GCTGGTGGAC AAAATTTTGT 960
GGCGCTCTGC GTCCCCTGAA GATCGTCTGG GGAATATTTT TCATCTTAGT TGCATTGCTG 1020
TTTGTAATTT CTCTTTTCTT GTCAAATTTA GATAAAGCTC TTCATTGAGT TGGAATAGAT 1080
TCTGGTTTCA TAATTTTGG AGCTAACCTG AGTAATCCAC TGAATATGCT TTTGCCTTTA 1140
CTACAAACAG TTTTCCCTCT TGATTATATT CTTATAACAA TTATTATTAT GTACTTTATT 1200
TTTACTTCAA TGGCAGGAAT TCGAAATATT GGCATATGGT TCTTTTGGAT TAGATTATAT 1260
AAAATCAGAA GAGGTAGAAC CAGGCCCCAA GCACTCCTTT TTCTCTGCAT GATACTTCTG 1320
CTTATTGTCC TTCACACTAG CTACATGATT TATAGTCTTG CTCCCCAATA TGTTATGTAT 1380
GGAAGCCAAA ATTACTTAAT AGAGACTAAT ATAACTTCTG ATAATCATAA AGGCAATTCA 1440
ACCTTTTCTG TGCCAAAAGAG ATGTGATGCA GATGCTCCTG AAGATCAGTG TACTGTTACC 1500
CGGACATACC TATTCCTTCA CAAGTTCTGG TTCTTCAGTG CTGCTTACTA TTTTGGTAAC 1560
TGGGCCTTTC TTGGGGTATT TTTGATTGGA TTAATTGTAT CCTGTTGTAA AGGGAAGAAA 1620
TCGGTTATTG AAGGAGTAGA TGAAGATTCA GACATAAGTG ATGATGAGCC CTCTGTCTAT 1680
TCTGCTTGAC AGCCTTCTGT CTTAAAGGTT TTATAATGCT GACTGAATAT CTGTTATGCA 1740
TTTTTAAAGT ATTAACTAA CATTAGGATT TGCTAACTAG CTTTCATCAA AAATGGGAGC 1800
ATGGCTATAA GACAACATA TTTTATTATA TGTTTCTGA AGTAACATTG TATCATAGAT 1860
TAACATTTTA AATTACCATA ATCATGCTAT GTAAATATAA GACTACTGGC TTTGTGAGGG 1920
AATGTTTGTG CAAAATTTTT TCCTCTAATG TATAATAGTG TTAAATTGAT TAAAAATCTT 1980
CCAGAATTAA TATTCCTTT TGTCACTTTT TGAACACATA ATAAATCATT TGTATCTGTG 2040
CCTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100
AAAAAAAAAA AAAAAAAAAA 2120

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(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

Met Lys Asn Gln Asn Gly Thr Phe Lys Asp Trp Ala Asn Ala Asn Val
 1             5             10             15

Ser Arg Gln Ile Glu Asp Thr Val Leu Tyr Gly Tyr Tyr Thr Leu Tyr
          20             25             30

Ser Val Ile Leu Phe Cys Val Phe Phe Trp Ile Pro Phe Val Tyr Phe
          35             40             45

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Tyr	Tyr	Glu	Glu	Lys	Asp	Asp	Asp	Thr	Ser	Lys	Cys	Thr	Gln	Ile	
50						55				60					
Lys	Thr	Ala	Leu	Lys	Tyr	Thr	Leu	Gly	Phe	Val	Val	Ile	Cys	Ala	Leu
65					70					75					80
Leu	Leu	Leu	Val	Gly	Ala	Phe	Val	Pro	Leu	Asn	Val	Pro	Asn	Asn	Lys
				85					90					95	
Asn	Ser	Thr	Glu	Trp	Glu	Lys	Val	Lys	Ser	Leu	Phe	Glu	Glu	Leu	Gly
			100					105					110		
Ser	Ser	His	Gly	Leu	Ala	Ala	Leu	Ser	Phe	Ser	Ile	Ser	Ser	Leu	Thr
		115					120					125			
Leu	Ile	Gly	Met	Leu	Ala	Ala	Ile	Thr	Tyr	Thr	Ala	Tyr	Gly	Met	Ser
	130					135					140				
Ala	Leu	Pro	Leu	Asn	Leu	Ile	Lys	Gly	Thr	Arg	Ser	Ala	Ala	Tyr	Glu
145					150					155					160
Arg	Leu	Glu	Asn	Thr	Glu	Asp	Ile	Glu	Glu	Val	Glu	Gln	His	Ile	Gln
				165					170					175	
Thr	Ile	Lys	Ser	Lys	Ser	Lys	Asp	Gly	Arg	Pro	Leu	Pro	Ala	Arg	Asp
			180					185					190		
Lys	Arg	Ala	Leu	Lys	Gln	Phe	Glu	Glu	Arg	Leu	Arg	Thr	Leu	Lys	Lys
		195					200					205			
Arg	Glu	Arg	His	Leu	Glu	Phe	Ile	Glu	Asn	Ser	Trp	Trp	Thr	Lys	Phe
	210					215					220				
Cys	Gly	Ala	Leu	Arg	Pro	Leu	Lys	Ile	Val	Trp	Gly	Ile	Phe	Phe	Ile
225					230					235					240
Leu	Val	Ala	Leu	Leu	Phe	Val	Ile	Ser	Leu	Phe	Leu	Ser	Asn	Leu	Asp
				245					250					255	
Lys	Ala	Leu	His	Ser	Ala	Gly	Ile	Asp	Ser	Gly	Phe	Ile	Ile	Phe	Gly
			260					265					270		
Ala	Asn	Leu	Ser	Asn	Pro	Leu	Asn	Met	Leu	Leu	Pro	Leu	Leu	Gln	Thr
		275					280					285			
Val	Phe	Pro	Leu	Asp	Tyr	Ile	Leu	Ile	Thr	Ile	Ile	Ile	Met	Tyr	Phe
	290					295					300				
Ile	Phe	Thr	Ser	Met	Ala	Gly	Ile	Arg	Asn	Ile	Gly	Ile	Trp	Phe	Phe
305					310					315					320
Trp	Ile	Arg	Leu	Tyr	Lys	Ile	Arg	Arg	Gly	Arg	Thr	Arg	Pro	Gln	Ala
				325					330					335	
Leu	Leu	Phe	Leu	Cys	Met	Ile	Leu	Leu	Leu	Ile	Val	Leu	His	Thr	Ser
			340					345					350		

Tyr Met Ile Tyr Ser Leu Ala Pro Gln Tyr Val Met Tyr Gly Ser Gln
 355 360 365
 Asn Tyr Leu Ile Glu Thr Asn Ile Thr Ser Asp Asn His Lys Gly Asn
 370 375 380
 Ser Thr Leu Ser Val Pro Lys Arg Cys Asp Ala Asp Ala Pro Glu Asp
 385 390 395 400
 Gln Cys Thr Val Thr Arg Thr Tyr Leu Phe Leu His Lys Phe Trp Phe
 405 410 415
 Phe Ser Ala Ala Tyr Tyr Phe Gly Asn Trp Ala Phe Leu Gly Val Phe
 420 425 430
 Leu Ile Gly Leu Ile Val Ser Cys Cys Lys Gly Lys Lys Ser Val Ile
 435 440 445
 Glu Gly Val Asp Glu Asp Ser Asp Ile Ser Asp Asp Glu Pro Ser Val
 450 455 460
 Tyr Ser Ala
 465

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTTCCGAAAT AAAAGATTTT GCAAACCACT TTCCTACGTA CGTCCACTGT AGTTTTTGCA 60
 GATACAACAC TAGCTGTAGC AAAGCCTATG TAAATCATAT GATGAGCTTT CATAGTAACC 120
 GTCCAAGCAA AAGGTTTTGT ATTTTAAAGA AGCATTCAGA AAATCTCCGG GGCATTACTC 180
 TAGTGTGCCT TAATTGTGAT TTCCTAAGTG ATGTTTCTGG CTTAGATAAT ATGGCTACAC 240
 ACTTAAGTCA ACATAAACT CATACTTGCC AAGTTGTAAT GCAGAAAGTT TCTGTTTGTA 300
 TCCCAACTTC TGAGCACCTT TCTGAATTAA AAAAAGAAGC TCCCGCAAAG GAACAAGAAC 360
 CTGTGTCTAA GGAAATTGCA AGACCTAACA TGGCTGAAAG AGAAACAGAA ACATCAAATT 420
 CTGAAAGTAA ACAAGATAAA GCTGCTTCTT CAAAAGAAAA AAATGGATGT AATGCAAATT 480
 CATTTGAAGG CTCATCAACA ACAAAAAGTG AAGAAAGCAT AACAGTTTCA GATAAGGAAA 540
 ATGAAACCTG TCTTGCAGAC CAGGAACTG GCTCAAAAAA CATCGTCAGT TGTGATTCAA 600
 ATATTGGTGC AGATAAAGTG GAAAAGAAAA AACAAATACA ACACGTTTGT CAGGAAATGG 660
 AGTTGAAGAT GTGCCAAAGT TCAGAAAACA TAATCTTATC TGATCAGATT AAAGATCACA 720
 ACTCCAGTGA AGCCAGATTT TCTTCAAAGA ATATTAAGGA TTTGCGATTA GCATCAGATA 780
 ATGTAAGCAT TGATCAGTTT TTGAGAAAAA GACATGAACC TGAATCTGTT AGTTCTGATG 840
 TTAGCGAGCA AGGCAGTATT CATTTGGAAC CTCTGACTCC ATCCGAGGTA CTTGAGTATG 900
 AAGCCACAGA GATTCTTCAG AAAGGTAGTG GTGATCCTTC AGCCAAGACT GATGAAGTAG 960
 TGTCTGATCA AACAGATGAC ATTCCTGGAG GAAATAACCC TAGCACAACA GAGGCAACAG 1020
 TAGACCTGGA AGATGAAAAA GAAAGAAGTT GAAATTAGTC ATTTTAAGTT TCAGTGTACC 1080

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AACGATAAGG GCATTTGGAA CAGTGCCTATC AGGTGAGCTC AGTGGTGCTG TTGTAGGTTT 1140
AGAAATGGAA ATATGTAAGG GAGGTCACAC ATACACTTTA CCTGTATGTT CAACCTATGT 1200
TATCAAACAA ATCAATTCAC CAATAATAGC ATGATTAGTA GGGATTCCCA AAAAGTTTTT 1260
AAAAACACGA ACAGGATTTT AATGATAATT AAATTTGCAG TGGAAAGGTC TCATTTAATG 1320
GTTTTCAAGG AAATGGGATT TGGTTGCTGA CATGAATTGA TGATATTAGT AATATTTATA 1380
AAGCCTTTCA AACTTCCATC AATCCTAAGC TAAAAATCTT TATTACCTGT ATATCCTTTT 1440
CAGTTAACTG AGAGGAAGGG ATTTGGAAAC CATGTACTTT TGGGGAGTAA TTGATTAAAA 1500
ACAATGGCTG ATTGGCATTG TTAATGAAGG CTTTATTTGT GAGGATGATG CTGGTAAATG 1560
GAGCATGCTT AGAGTACTAA ATTGATCTAA TGAGAATTTG GATGAACATA AACTTAATTT 1620
TGGATTTAAT ATAACATTCC AGTCAGACGC ATGTAAACAG AATATTTGAA TCTTTGTACC 1680
TCCATACAAG TGTTAGCCTG CCAGGCTGTA AGCTTACCTT AATTAAACTT TCAGTGAAAG 1740
TGGAATTATT AAGATATAAA TTTATATTTG TGCTTTTGT CAGTGTGTAA GCTGTGTAGA 1800
AATTCCTTTGA TGTATTAGTT GTATTAATGT AAAGTAGAAA CCCATTGTTG AAACCTCTGT 1860
AGCTATTATG CTTTTAATAT TGTTTTAATG ATCTTCCTTA GAAATAGGCC CATAAAAATG 1920
GTCTGGAAGC CAAACCAAAG TATGGTATAA TGTAGATATT GTAAAGCAGT AAACGAAAAA 1980
CATGTCCTGG CATGTATTCA GCCATGTTTA AGTGACTTTT CTGTAATTGT AAAATAAAAA 2040
CTTCAAATGG GACCTAAAC AGTGATGTAA AAGAACTGGT TTTGGAAATT TAGCCTAATT 2100
TATCTATAAG ATGGCTGCTA AATTGATTTT TCAGTTCTTT TTATCATCTA GAATATAATA 2160
GATATAGAAA TGAATAATAT GAAGAACAGT AGTTTGCTTT GAAATACTAA TAAACTTTTA 2220
TTTAAATGTC TTCATTTTTA CTTCTTAAAA TGTGCTTTGG ATTCTTAAAT TTTGTTTCAC 2280
TGAATGTTCA ATGTTTTTAA TGCGGATTAA AATACTCTGC TGTATATAGT AGTTTTTGAG 2340
TAAATATTTG CAATAAAAAAT CTGCCCCCGA ATAAAAAAA AAAAAAAAAA AAAAAAAAAA 2400
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAAAAA AAAAAAAAAA AAAAAA 2487

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(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

Met Met Ser Phe His Ser Asn Arg Pro Ser Lys Arg Phe Cys Ile Phe
 1             5             10             15

Lys Lys His Ser Glu Asn Leu Arg Gly Ile Thr Leu Val Cys Leu Asn
 20             25             30

Cys Asp Phe Leu Ser Asp Val Ser Gly Leu Asp Asn Met Ala Thr His
 35             40             45

Leu Ser Gln His Lys Thr His Thr Cys Gln Val Val Met Gln Lys Val
 50             55             60

Ser Val Cys Ile Pro Thr Ser Glu His Leu Ser Glu Leu Lys Lys Glu
 65             70             75             80

Ala Pro Ala Lys Glu Gln Glu Pro Val Ser Lys Glu Ile Ala Arg Pro
 85             90             95

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Asn Met Ala Glu Arg Glu Thr Glu Thr Ser Asn Ser Glu Ser Lys Gln
 100 105 110
 Asp Lys Ala Ala Ser Ser Lys Glu Lys Asn Gly Cys Asn Ala Asn Ser
 115 120 125
 Phe Glu Gly Ser Ser Thr Thr Lys Ser Glu Glu Ser Ile Thr Val Ser
 130 135 140
 Asp Lys Glu Asn Glu Thr Cys Leu Ala Asp Gln Glu Thr Gly Ser Lys
 145 150 155 160
 Asn Ile Val Ser Cys Asp Ser Asn Ile Gly Ala Asp Lys Val Glu Lys
 165 170 175
 Lys Lys Gln Ile Gln His Val Cys Gln Glu Met Glu Leu Lys Met Cys
 180 185 190
 Gln Ser Ser Glu Asn Ile Ile Leu Ser Asp Gln Ile Lys Asp His Asn
 195 200 205
 Ser Ser Glu Ala Arg Phe Ser Ser Lys Asn Ile Lys Asp Leu Arg Leu
 210 215 220
 Ala Ser Asp Asn Val Ser Ile Asp Gln Phe Leu Arg Lys Arg His Glu
 225 230 235 240
 Pro Glu Ser Val Ser Ser Asp Val Ser Glu Gln Gly Ser Ile His Leu
 245 250 255
 Glu Pro Leu Thr Pro Ser Glu Val Leu Glu Tyr Glu Ala Thr Glu Ile
 260 265 270
 Leu Gln Lys Gly Ser Gly Asp Pro Ser Ala Lys Thr Asp Glu Val Val
 275 280 285
 Ser Asp Gln Thr Asp Asp Ile Pro Gly Gly Asn Asn Pro Ser Thr Thr
 290 295 300
 Glu Ala Thr Val Asp Leu Glu Asp Glu Lys Glu Arg Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

TTTATTTTTTC	AAATCATAAT	TTTAAAATGA	TAGATACCAT	TTTGTGATAA	CAACAATTCA	60
GAAAACAATT	TTCTATCCTC	TTAGTTGAAA	GAATGTAGGT	ACAGTTTGGA	TACTTGTAAT	120
TTAATTTTTAG	AGTAAACATC	TGCATTATAC	TCTTATAGAT	AATAGAAATTA	TTTAGTTAAG	180
AAATTCTTTA	CAGTAAATGA	GATAATGTGT	GAAAAAGTAT	TTTGTAAATG	CTGAGGATTC	240
TACAAATGAT	AGTTGTTATT	TTTATGTGTA	TTTGTAAAGAT	CATGTCCATT	TCATGAATAT	300
AGGACTTCAC	ATAAAAAAAG	ACTTTCTCAA	GACAACCTTA	TATTCTAGTA	TTTTTCTGTT	360
GTAAAAAGTA	TTAACTATTT	ACTTTTATTT	TGTTATACAT	TTATTTTAAT	ATCCATGTGT	420
TTATTATAGT	AAATTTGAAA	TGAAATCCTG	AAAAACAGAA	TTTTTTTAAA	CACAGACCTC	480
ACACCAATAT	TAATTTTTTTC	TCTACATAAT	TTAAAACTAC	ATAAATTAAG	TACTTAAAAT	540
TTATATTGAA	GGCCACCAAG	AACTTAGGTT	GAATCTTAGA	AAATTTAAAT	AACTATTTTT	600
AAAGTTACCC	AACTTAATAT	TTTAATTTTT	TAATATTTAT	CTTCCTTTAC	TAATTCCTGA	660
TAAATAATAG	CATTAGACTT	GATAAAATAA	AAAAGAATTT	TAGAGTAGAA	TTAATATATC	720
AAAAGGGGTA	TATCAACCAA	ATTGGTGTCA	GATTGTATTTC	ATTCTCTCAT	CACATAAAGA	780
TTTTTCTTTT	GATAGGTGAT	GCTCATATGA	ACCTTTGGTT	TAGAATCTAT	ATATGTACAT	840
GTGTATGTAT	GATAGATAGTA	TGGTTGTATA	CACACATATA	TACCAAAACAC	CATGAATTTT	900
AGCAGTCTGT	GATGATCAGC	AAAAAAGCAC	ATAAAGTAAA	ATTAGTTGAC	CATGCTAAAT	960
TCAATTCTGG	AATTTTTTTT	TATTTGGGCA	TTTCTAGAAC	TTTTTACATT	TGAAAGTACA	1020
TGATGAGTAT	TAGTAACGAT	GACTTATGTA	TAATCAGAAT	CTTTATGACA	ATTTAGTTTT	1080
ACAAGGTCAG	AAGAGATGAG	TTTGCTAAAC	CCAGCTGTGA	TACCTCAGTT	GGAAAGGGAA	1140
TTCAAAAGTA	TGCTTTGTAG	AACAGAAAAG	TATAGTTTTT	TTTTCATGAA	CTTTAATCAT	1200
TTTCTGTTTT	TCTCTATGTT	GAGTCAGCTA	CAAAAGTGGT	CTAATTTTTA	CAACAGTAGA	1260
ACTTCCTCCT	TTTCTACTGT	AATCTTCCCA	CTGACTTTAC	TGCACAGGTA	TGAAATACTA	1320
GTGTATTGGA	TCTTCAGTAA	CCTTTTTTAT	TCCTAGATGA	TTGAAATATA	GGTATTTACT	1380
CCATTTAAAC	CAGGTGATAA	GATGATGTAA	ATACTCAGGG	AGGGTATTAA	CTTGTTACTT	1440
TTGCTCGTTT	GGGGTGTAAG	GTGCCATGAC	TGAATAATCT	TCAATTCATG	ATTCTAGAGT	1500
AAGTTTAATT	TGGAAAAAGG	GGCTTCACAC	ATGGTGGTGG	TTGAACATTG	ATTCTTTTAT	1560
ACTTAAAAAG	ATGAAAAATG	TTTGTGGACT	GATACATTTT	ATCTTACTGA	ATATGAATTG	1620
TTTATGTATC	TCTACTGTCA	AATAGCCTTT	TTGAAACTCA	GGAAAGACAA	AGGTTCAATT	1680
ACACCACTTT	TGTCAATAAG	CAAACCAGGT	ATTTTTTTTT	TCTCCTGTTG	TCTGGATATG	1740
GCAATAGATT	TTTTAAATTT	CTGTGAGAAC	CCATATATGA	AAAGAGAGGA	GTTGAATTGT	1800
GTGTGCCTTT	TATGTCTTGA	GATTTATATG	TGGAAAAGAC	GACATCTACT	TCAAACCTGA	1860
TTTTTTTTCGT	TTTTTTTTTT	TTTTTGGGGA	AGGGGGGAGA	ACGGGGTCTT	GCTCTGTCTG	1920
CCAGGCTGGA	GTGCAGTGGC	GCGATCTCAG	CTGACTGCAA	CCTCCACCTC	CCGGGTTCAA	1980
GGGATTCTGC	CTCAGCCTCC	CGAGTAGCTG	AGACCACAGG	TGCGTGCCAC	CACACCCGGC	2040
TAATTTTTTT	GTATTTTTAG	TAGAGACGGG	GTTTAGTAGA	GACGGATCAC	TCCTGACCAT	2100
GTGATCCGCG	CACCTCGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCGTGAGC	CACCACCCCC	2160
GGCCTGTATT	TTCAAGAGAG	AGAGCTTGGT	GTTTTTGTGG	TGCCAAGTGG	TAAGATAATG	2220
TCTCTTTGAG	GCTTCCATAG	GACTGCCTTT	ATTTTAGTAA	ACTCAAGACA	CCAGTTAACC	2280
TCAACAGAGT	TTTGGCCTTA	TTAGAATTTG	TTGTGCATCT	TATTGAAAGC	CAGGTTTACA	2340
TCACCTCACC	CCATTATTCT	TTTTAGTTAA	ATAAATTTAC	CATGCCAAGT	AACCAGAATG	2400
GAGCAAATTG	GTTGATCTTT	AAGGCAGTAG	GTTTGACTAG	CTAGCTATCA	TTATTGTCAC	2460
ATCTAATGCT	AGGCACCAGA	AACCATTGTA	GCCAGGAGTG	TGAATGAATA	ATTCCCAGAG	2520
ACACTTTAGA	CATTTTTTAA	TGTTTTATAT	GACATTTTAC	ATTTGTGTGA	TTGCCTTAGA	2580
TATTAAATTT	TCCTAGTGCT	GATAAAAACA	GCAACATTCA	TAACTTATTT	TATATATTGT	2640
TCCAAAGAAA	AGAATTTGTT	TTAATGGTTT	CAAAATAACT	GCACCTGAAT	TTGTTTATGT	2700
GCCTTAAGTT	CTCTAGTGCT	ATTTCAACTT	TTTTTTCAAT	CTAAATGAAG	CTTACCTTAG	2760
ATAAGGTTCA	TATTTGTTTC	CTATAGAGTA	AATAAACTTC	CCCTTCTTAA	ATTGTGTAAT	2820
AAGCACCAAC	GTGTGGTTGC	TTGGCAGAAT	GAGAATGTTA	AGGGAGATTG	TTGGATGTTT	2880
GGAGTTTCAT	TATATTTTTT	GTTTTTATTT	TTTGATACCT	AGGTGCTTTT	TAAAATATTC	2940
AGACAAATAT	CTATCTTACA	TTGATTAAAC	CCGTGTAAAT	TCATTTGCAG	TATCTACATC	3000
GAATGTCAAA	AAAGTATACT	TATTTTTGTT	CCATACTTAT	GTACAATTTT	TTCCCTCTTC	3060
AGGCTTTTTT	ATTTACCTTT	TTGAAAAAGC	ACTTACTCTC	CCCTTCCCTA	TCACCCCTCC	3120
CCCAAGGTTT	CTTTATTTAA	ATTTTTATTG	AGAGTTGTTG	GAGCTCTAAG	ACAATACAAA	3180
TTTAGAGTTG	AACAAAAGTA	TAATCTGCTT	TACAACATAG	ATAGACCTAA	GGTCATTTGC	3240
TTTCAATTAG	AGGCTCCAGA	GTCTTCATAG	TGGAAAGAAT	GCTTTGTATT	TAATTGTTCT	3300
TAGTTAAGTT	GATGACCGTG	AATACTTACT	TACATGTTTT	GTTTAAATAT	ACTTCTTGCA	3360

TAGTTTAAATT TTTTAAAAGT TGTATCTAAT AAAATGTCTT TTAACCATTA TTAAGTGGCT 3420
 ATATGGTTGT ATTAATTTT GTTTACGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3480
 AAAAAAAAAA AAAAA 3495

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Lys Lys Tyr Thr Tyr Phe Cys Ser Ile Leu Met Tyr Asn Phe
 1 5 10 15
 Phe Pro Leu Gln Ala Phe Ser Phe Thr Phe Leu Lys Lys His Leu Leu
 20 25 30
 Ser Pro Ser Leu Ser Pro Leu Pro Gln Gly Phe Phe Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GTTGATCCAT CTGAGAAAGG GATCATGAAC TAGACAGAAT GAACAGCCTT AGAGGCACAG 60
 ACTCTTGAAC GGGACGGTGG TGGTATGACT AGTGCAGAGT GTTTAGAGAT CACTCAGTTT 120
 TTAAAGACTG GCCTTTATCG TGTCTCAGTG CAGCCGAGGC AGAGCCTTTG AAGGATGCGA 180
 TGTTGTGATT CTTACTAATC TAGTCCAGCC GCTGAGGTGA CTTTCAACGG CAGACCGTCT 240
 CCTGAGCGCC CCAGGTAGAA TTTCAAAGT CTCCGGGACC ATTATGGCAG TCAAGTGGAC 300
 GGGTGGGCAT TCTTCTCCTG TCCTCTGCCT GAATGCAAGT AAAGAAGGGC TGCTGGCTTC 360
 TGGAGCAGAG GGCGGAGATC TCACGGCTTG GGGTGAAGAT GGAAGTCCAT TAGGACACAC 420
 GCGGTTCCAA GGGGCTGATG ATGTTACCAG TGTCTTATTT TCTCCCTCCT GTCCCACCAA 480
 GCTCTATGCC TCACATGGAG AAACCATTAG TGTACTGGAT GTCAGGTCCC TCAAAGATTC 540
 CTTGGACCAT TTTCATGTGA ATGAAGAAGA AATCAATTGT CTTTCATTGA ATCAAACGGA 600
 AAACCTGCTG GCTTCTGCTG ACGACTCTGG GGCAATCAAA ATCCTAGACT TGGAAAACAA 660
 GAAAGTTATC AGATCCTTGA AGAGACATTC CAATATCTGC TCCTCAGTGG CTTTTCGGCC 720
 TCAGAGGCCT CAGAGCCTGG TGTCATGTGG ACTGGATATG CAGGTGATGC TGTGGAGTCT 780
 TCAAAAAGCC CGACCACTCT GGATTACAAA TTTACAGGAG GATGAAACAG AAGAAATGGA 840
 AGGCCACAG TCACCTGGTC AGCTCTTAAA CCCTGCCCTA GCCCATTTCTA TCTCTGTGGC 900

TTCGTGTGGT AATATTTTGA GTTGTGGTGC AGAAGATGGT AAGGTTTCGAA TCTTTCGGGT 960
 GATGGGAGTT AAGTGTGAAC AGGAACTGGG ATTTAAGGGC CACACTTCAG GGGTATCCCA 1020
 GGTCTGCTTT CTCCCAGAAT CCTATTTGCT GCTTACTGGA GGAATGATG GGAAGATCAC 1080
 GTTGTGGGAT GCAAACAGTG AAGTTGAGAA AAAACAGAAG AGTCCCACAA AACGTACCCA 1140
 CAGGAAGAAA CCTAAAAGAG GAACTTGCAC CAAGCAGGGT GGAAATACTA ACGCTTCAGT 1200
 AACAGATGAG GAAGAACATG GCAACATTTT ACCGAAGCTA AATATTGAAC ATGGAGAAAA 1260
 AGTGAAGCTG CTCTTGGGTA CAAAAATAAA GGGACACCAA AATATATTAG TAGCTGATCA 1320
 AACTAGTTGT ATATCTGTAT ACCCCTTAAA TGAATTTTAA ATCCAATAAA AACATTTGAA 1380
 GAAAAAAAAA AAAAAAAAAA 1398

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met	Ala	Val	Lys	Trp	Thr	Gly	Gly	His	Ser	Ser	Pro	Val	Leu	Cys	Leu	1	5	10	15
Asn	Ala	Ser	Lys	Glu	Gly	Leu	Leu	Ala	Ser	Gly	Ala	Glu	Gly	Gly	Asp	20	25	30	
Leu	Thr	Ala	Trp	Gly	Glu	Asp	Gly	Thr	Pro	Leu	Gly	His	Thr	Arg	Phe	35	40	45	
Gln	Gly	Ala	Asp	Asp	Val	Thr	Ser	Val	Leu	Phe	Ser	Pro	Ser	Cys	Pro	50	55	60	
Thr	Lys	Leu	Tyr	Ala	Ser	His	Gly	Glu	Thr	Ile	Ser	Val	Leu	Asp	Val	65	70	75	80
Arg	Ser	Leu	Lys	Asp	Ser	Leu	Asp	His	Phe	His	Val	Asn	Glu	Glu	Glu	85	90	95	
Ile	Asn	Cys	Leu	Ser	Leu	Asn	Gln	Thr	Glu	Asn	Leu	Leu	Ala	Ser	Ala	100	105	110	
Asp	Asp	Ser	Gly	Ala	Ile	Lys	Ile	Leu	Asp	Leu	Glu	Asn	Lys	Lys	Val	115	120	125	
Ile	Arg	Ser	Leu	Lys	Arg	His	Ser	Asn	Ile	Cys	Ser	Ser	Val	Ala	Phe	130	135	140	
Arg	Pro	Gln	Arg	Pro	Gln	Ser	Leu	Val	Ser	Cys	Gly	Leu	Asp	Met	Gln	145	150	155	160
Val	Met	Leu	Trp	Ser	Leu	Gln	Lys	Ala	Arg	Pro	Leu	Trp	Ile	Thr	Asn	165	170	175	
Leu	Gln	Glu	Asp	Glu	Thr	Glu	Glu	Met	Glu	Gly	Pro	Gln	Ser	Pro	Gly				

180	185	190
Gln Leu Leu Asn Pro Ala Leu Ala His Ser Ile Ser Val Ala Ser Cys		
195	200	205
Gly Asn Ile Phe Ser Cys Gly Ala Glu Asp Gly Lys Val Arg Ile Phe		
210	215	220
Arg Val Met Gly Val Lys Cys Glu Gln Glu Leu Gly Phe Lys Gly His		
225	230	235
Thr Ser Gly Val Ser Gln Val Cys Phe Leu Pro Glu Ser Tyr Leu Leu		
245	250	255
Leu Thr Gly Gly Asn Asp Gly Lys Ile Thr Leu Trp Asp Ala Asn Ser		
260	265	270
Glu Val Glu Lys Lys Gln Lys Ser Pro Thr Lys Arg Thr His Arg Lys		
275	280	285
Lys Pro Lys Arg Gly Thr Cys Thr Lys Gln Gly Gly Asn Thr Asn Ala		
290	295	300
Ser Val Thr Asp Glu Glu Glu His Gly Asn Ile Leu Pro Lys Leu Asn		
305	310	315
Ile Glu His Gly Glu Lys Val Asn Trp Leu Leu Gly Thr Lys Ile Lys		
325	330	335
Gly His Gln Asn Ile Leu Val Ala Asp Gln Thr Ser Cys Ile Ser Val		
340	345	350
Tyr Pro Leu Asn Glu Phe		
355		

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

CCGGAGGTAG CTACCACGGC CTGTGTCAAC GACTAAAGCT CCAGTACAGC GGCGCCCTCA 60
GACAGCTGGG AGGGTGGCTC TGGCCGGGAG CGGCGGCCGG TGAGCTACCG CGAGGAGGAG 120
CGGCGGAGGC GACCTCGGCC CGGCCCTGCA CTGGCCGCCC GGCAGGCGCG ACATGAGCCT 180
GGTCTGGCAT CCGCGGGATG CTCCTTAAGC CCCTTCTCCG GCTGTTAACC TCCGGGGAAC 240
GGTTGTGACC ACACCGACAC GTATTTTACA GATAAATCAT TCTTGCGGCG GCGGGTCGAA 300
CACGTTTATT TATTTTAT TTTCTCAACA AGCTTTTACC CAGCACCTGT CCAGTGAAAC 360
AACTTGATAA TCGTTTCGAG GGGCGTCCGC CGGGTTAGGA AGCCACTGCC TGGCAGCTTG 420
TGGAAGCCTC ATTTGCAAAG CCACCCCTCA GATGTTTGA AGATCGTGAC GTCTTGTAAC 480

```

TAGCAGTGTG TGCACAGAAT CCTACTCAAG GAACGTCTTG GCCCAGCGAT GCAAAGAAGT 540
 GAAGTTTCAA GCTGGAAGAG CCTGTATTGT CCTCACAATA GTATAGAAGA ATTCAGAGAGA 600
 GGAGAGAGAG ACAGCACCGA ATGAAGACTG TAAAAGAAAA GAAGGAATGC CAGAGATTGA 660
 GAAAATCTGC CAAGACTAGG AGGGTAACCC AGAGGAAACC GTCTTCAGGG CCTGTTTGCT 720
 GGCTATGCCT TCGAGAACCT GGGGATCCCG AAAAATTAGG GGAATTTCTT CAGAAAGACA 780
 ATATCAGCGT GCATTATTTT TGTCTTATCT TATCTAGTAA GCTGCCTCAG AGGGGCCAGT 840
 CCAACAGAGG TTTCCATGGA TTTCTGCCTG AAGACATCAA AAAGGAGGCA GCCCGGGCTT 900
 CTAGGAAGAT CTGCTTTGTG TGCAAGAAAA AGGGAGCTGC TATCAACTGC CAGAAGGATC 960
 AGTGCCTCAG AAACCTCCAT CTGCCTTGTG GCCAAGAAAG GGGTTGCCTT TCACAATTTT 1020
 TTGGAGAGTA CAAATCATT TGTGACAAAC ATCGCCCAAC ACAGAACATC CAACATGGGC 1080
 ATGTGGGGGA GGAAAGCTGC ATCTTATGTT GTGAAGACTT ATCCCAACAG AGTGTGAGA 1140
 ACATCCAGAG CCCGTGTTGT AGTCAAGCCA TCTACCACCG CAAGTGCATA CAGAAATATG 1200
 CCCACACATC AGCAAAGCAT TTCTTCAAAT GTCCACAGTG TAACAATCGA AAAGAGTTTC 1260
 CTCAAGAAAT GCTGAGAATG GGAATTCATA TTCCAGACAG AGATGCTGCC TGGGAAGTGC 1320
 AGCCAGGGGC TTTCTCAGAC TTATATCAGC GCTATCAGCA CTGTGATGCC CCCATCTGTC 1380
 CGTATGAACA AGGCAGAGAC AGCTTTGAGG ATGAAGGGAG GTGGTGCCTC ATTCTGTGTG 1440
 CTACATGCGG ATCCCACGGA ACCCACAGGG ACTGCTCCTC TCTTAGATT AACAGTAAGA 1500
 AATGGGAGTG TGAGGAGTGT TCACCTGCTG CAGCCACAGA CTACATACCT GAAAACCTCAG 1560
 GGGACATCCC TTGCTGCAGC AGCACCTTCC ACCCTGAGGA ACATTTCTGC AGAGACAACA 1620
 CTTTGGAGA GAATCCGGGC CTTTCTTGGG CTGATTGGCC AGAACCTTCC TTATTAGAAA 1680
 AGCCAGAGTC CTCTCGTGGC AGGAGGAGCT ACTCCTGGAG GTCCAAGGGT GTCAGAATCA 1740
 CTAACAGCTG CAAAAAATCC AAGTAACACC TTCTGAGTAG CTGCTGTCCC ACACAATAGG 1800
 GTATGAAGCT GCGCTCCTCC ATCGGGTTTG GGGAGGGAGC ACTCTGGGAC TGTGAGACAA 1860
 GGAAGCAGGG CCAGCAGTGA GACTATGAGC CAAGCAAAGA GAAGTCTCAG TGGAGCATGA 1920
 GGAGGGAGCA GTCCAGATGC CAACAAGGAA ATGCGTTTAT GGCTACAAGA GTGCCTCTGC 1980
 TTTCTCCTCC TCTCCTCCCA CCAAGGATTC TTCCACCTTA ATCTTGTTTT CATATGCCTC 2040
 TTCTTACTTC ACCCATGTTT GTTGTTATGC AAATAAAGGT TTTCTCTCCC AAAAAAAAAA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2132

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Lys Thr Val Lys Glu Lys Lys Glu Cys Gln Arg Leu Arg Lys Ser
 1 5 10 15
 Ala Lys Thr Arg Arg Val Thr Gln Arg Lys Pro Ser Ser Gly Pro Val
 20 25 30
 Cys Trp Leu Cys Leu Arg Glu Pro Gly Asp Pro Glu Lys Leu Gly Glu
 35 40 45
 Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr Phe Cys Leu Ile Leu
 50 55 60
 Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn Arg Gly Phe His Gly
 65 70 75 80
 Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala Arg Ala Ser Arg Lys

85

90

95

Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala Ile Asn Cys Gln Lys
 100 105 110
 Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys Gly Gln Glu Arg Gly
 115 120 125
 Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser Phe Cys Asp Lys His
 130 135 140
 Arg Pro Thr Gln Asn Ile Gln His Gly His Val Gly Glu Glu Ser Cys
 145 150 155 160
 Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser Val Glu Asn Ile Gln
 165 170 175
 Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg Lys Cys Ile Gln Lys
 180 185 190
 Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys Cys Pro Gln Cys Asn
 195 200 205
 Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg Met Gly Ile His Ile
 210 215 220
 Pro Asp Arg Asp Ala Ala Trp Glu Leu Glu Pro Gly Ala Phe Ser Asp
 225 230 235 240
 Leu Tyr Gln Arg Tyr Gln His Cys Asp Ala Pro Ile Cys Pro Tyr Glu
 245 250 255
 Gln Gly Arg Asp Ser Phe Glu Asp Glu Gly Arg Trp Cys Leu Ile Leu
 260 265 270
 Cys Ala Thr Cys Gly Ser His Gly Thr His Arg Asp Cys Ser Ser Leu
 275 280 285
 Arg Phe Asn Ser Lys Lys Trp Glu Cys Glu Glu Cys Ser Pro Ala Ala
 290 295 300
 Ala Thr Asp Tyr Ile Pro Glu Asn Ser Gly Asp Ile Pro Cys Cys Ser
 305 310 315 320
 Ser Thr Phe His Pro Glu Glu His Phe Cys Arg Asp Asn Thr Leu Glu
 325 330 335
 Glu Asn Pro Gly Leu Ser Trp Thr Asp Trp Pro Glu Pro Ser Leu Leu
 340 345 350
 Glu Lys Pro Glu Ser Ser Arg Gly Arg Arg Ser Tyr Ser Trp Arg Ser
 355 360 365
 Lys Gly Val Arg Ile Thr Asn Ser Cys Lys Lys Ser Lys
 370 375 380

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```
GTCACGTGGA ACCTCTTAAT CTCAGCATCC GGAGCTCCAG GAAGGGAAAA TTTCAAGTCA 60
GATAGAATTC TATATATACC ATTTCTTTGG AACCTTCAGC CCTCAAGATT CCAACATCAT 120
GACCTCAGTT TCAACACAGT TGTCTTAGT CCTCATGTCA CTGCTTTTGG TGCTGCCTGT 180
TGTGGAAGCA GTAGAAGCCG GTGATGCAAT CGCCCTTTTG TTAGGTGTGG TTCTCAGCAT 240
TACAGGCATT TGTGCCTGCT TGGGGGTATA TGCACGAAAA AGAAATGGAC AGATGTGACT 300
TTGAAAGGCC TACTGAGTCA AACCTCACCC TGAAAACCTT TGCGCTTTAG AGGCTAAACC 360
TGAGATTTGG TGTGTGAAAG GTTCCAAGAA TCAGTAAATA AGGGAGTTTC ACATTTTTC 420
TTGTTTCCAT GAAATGGCAA CAAACATACA TTTATAAATT GAAAAAAAAA TGTTTCTTT 480
ACAACAAATA ATGCACAGAA AAATGCAGCC TATAATTTGC TAGTTAGGTA GTCAAAGAAG 540
TAAGATGGCT GAAATTTACA TAAGTAATAT TTCATAATCT TAGAATTCTC TCAAAGCATG 600
TGAAATAGGA AGAAGGAAGT TCTTGCCCGA AATCTTAGGA AATCACCCT GTTCGGTTAT 660
AATCACTGCC TCCTGAATCG TTGAGGAGTC TTTTAAATTA GATTTTGTG TTGTTGTCTC 720
CCAAGTTAAT ATTATATTTA GATATCAGAG AGTCAGGCAA AAAGGAAAAC TTTTATCTCT 780
AGGGAAAAAA CATTTAGAAA AATGTATTCA GTGTATCTAA TACTGAAATG CGGAAAAAAA 840
TTTAATGTTA AAAAAAACT ATAGACATTG ACATGGAAAA GAGATTTAAT GTTTTGAAAA 900
AAAAACTTTA TATTAAGTGA GTAACATCCT CCTGATGAGA AGTACTATAT TAAATATAAA 960
CCCATTATGT TATAAAAAAA AAAA                                     984
```

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```
Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
 1                      5                      10                      15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
                20                      25                      30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu
          35                      40                      45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met
 50                      55
```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

G TTCCTACAG CGGTGAGAGT GAAATGTG

28

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

C CGGATACACC AAAGTCTCAT CCCTAAAT

28

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

G AGCTAGTGT GAAGGACAAAT AAGCAGAA

28

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GTCGCTAACA TCAGAACTAA CAGATTCA

28

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGATACTGC AAATGAATTT ACACGGGT

28

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GTCACACTTA ACTCCCATCA CCCGAAAG

28

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCTGAGGCAC TGATCCTTCT GGCAGTTG

28

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TGAGGGCTGA AGGTTCCAAA GAAATGGT

28

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGCTTTTTTT TTTTTTTTGA CAAGATGGCG GCAGGAGGCA GTGGCGTTGG TGGGAAGCGC 60
 AGCTCGAAAA GCGATGCCGA TTCTGGTTTC CTGGGGCTGC GGCCCACTTC GGTGGACCCA 120
 GCGCTGAGGC GGCGGCGGCG AGGCCCAAGA AATAAGAAGC GGGGCTGGCG GCGGCTTGCT 180
 CAGGAGCCGC TGGGGCTGGA GGTTGACCAG TTCCTGGAAG ACGTGCGGCT ACAGGAGCGC 240
 ACAGAGCGTG GCTTGTTGTC AGAGGCCCCA AATGAAAAAC TCTTCTTCGT GGACACTGGC 300
 TCCAAGGAAA AAGGGCTGAC AAAGAAGAGA ACCAAAGTCC AGAAGAAAGTC ACTGCTTCTC 360
 AAGAAACCCC TTCGGTTGA CCTCATCCTC GAGAACACAT CCAAAGTCCC TGCCCCCAA 420
 GACGTCCTCG CCCACCAGGT CCCCAACGCC AAGAAGCTCA GGCGGAAGGA GCAGCTATGG 480
 GAGAAGCTGG CCAAGCAGGG CGAGCTGCCC CGGGAGGTGC GCAGGGCCCA GGCCCGGCTC 540
 CTCAACCCTT CTGCAACAAG GGCCAAGCCC GGGCCCCAGG ACACCGTAGA GCGGCCCTTC 600
 TACGACCTCT GGGCCTCAGA CAACCCCTG GACAGGCCGT TGGTTGGCCA GGATGAGTTT 660
 TTCCTGGAGC AGACCAAGAA GAAAGGAGTG AAGCGGCCAG CACGCCTGCA CACCAAGCCG 720
 TCCCAGGCGC CCGCCGTGGA GGTGGCGCCT GCCGGAGCTT CCTACAATCC ATCCTTTGAA 780
 GACCACCAGA CCCTGCTCTC AGCGGCCAC GAGGTGGAGT TGCAGCGGCA GAAGGAGGCG 840
 GAGAAGCTGG AGCGGCAGCT GGCCCTGCCC GCCATGGAGC AGGCCGCCAC CCAGGAGTCC 900
 ACATTCCAGG AGCTGTGCGA GGGGCTGCTG GAGGAGTCGG ATGGTGAGGG GGAGCCAGGC 960
 CAGGGCGAGG GGCCGGAGGC TGGGGATGCC GAGGTCTGTC CCACGCCCGC CCGCCTGGCC 1020
 ACCACAGAGA AGAAGACGGA GCAGCAGCGG CGGCGGGAGA AGGCTGTGCA CAGGCTGCGG 1080
 GTACAGCAGG CCGCGTTGCG GGCCGCCCGG CTCCGGCACC AGGAGCTGTT CCGGCTGCGC 1140
 GGGATCAAGG CCCAGGTGGC CCTGAGGCTG GCGGAGCTGG CGCGGCGGCG GAGGCGGCGG 1200
 CAGGCGCGGC GGGAGGCTGA GGCTGACAAG CCCCGAAGGC TGGGACGGCT CAAGTACCAG 1260
 GCACCTGACA TCGACGTGCA GCTGAGCTCG GAGCTGACAG ACTCGCTCAG GACCTGAAG 1320
 CCCGAGGGA ACATCCTTCG AGACCGTTTC AAGAGCTTCC AGAGGAGGAA TATGATCGAG 1380
 CCTCGAGAGA GAGCCAAGTT CAAACGCAAG TACAAGGTGA AGCTGGTGGG GAAGCGGGCG 1440
 TTCCGTGAGA TCCAGTTGTA GCTGCCATCA GATGCCGGAG ACTCGCCCTT CAATAAAAAA 1500
 TCTCTTCTAG CTGAAAAAAA AAAAAAAA 1528

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser
1 5 10 15
Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
20 25 30
Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
35 40 45
Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
50 55 60
Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
65 70 75 80
Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
85 90 95
Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
100 105 110
Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
115 120 125
Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
130 135 140
Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
145 150 155 160
Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
165 170 175
Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
180 185 190
Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
195 200 205
Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
210 215 220
Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val
225 230 235 240

Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr
245 250 255

Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala
260 265 270

Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Met Glu Gln Ala Ala
275 280 285

Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu
290 295 300

Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly
305 310 315 320

Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys
325 330 335

Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg
340 345 350

Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu
355 360 365

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
370 375 380

Leu Ala Arg Arg Arg Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala
385 390 395 400

Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
405 410 415

Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
420 425 430

Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
435 440 445

Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
450 455 460

Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
465 470 475

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

ACAAGATGGC GGCGCCGAAG GGGAGCCTCT GGGTGAGGAC CCAACTGGGG CTCCCGCCGC 60
TGCTGCTGCT GACCATGGCC TTGGCCGGAG GTTCGGGGAC CGCTTCGGCT GAAGCATTG 120
ACTCGGTCTT GGGTGATACG GCGTCTTGCC ACCGGGCCTG TCAGTTGACC TACCCCTTGC 180
ACACCTACCC TAAGGAAGAG GAGTTGTACG CATGTCAGAG AGGTTGCAGG CTGTTTTCAA 240
TTTGTGAGTT TGTGGATGAT GGAATTGACT TAAATCGAAC TAAATTGGAA TGTGAATCTG 300
CATGTACAGA AGCATATTCC CAATCTGATG AGCAATATGC TTGCCATCTT GGTTGCCAGA 360
ATCAGCTGCC ATTCGCTGAA CTGAGACAAG AACAACCTAT GTCCCTGATG CCAAAAATGC 420
ACCTACTCTT TCCTCTAACT CTGGTGAGGT CATTCTGGAG TGACATGATG GACTCCGCAC 480
AGAGCTTCAT AACCTCTTCA TGGACTTTTT ATCTTCAAGC CGATGACGGA AAAATAGTTA 540
TATTCCAGTC TAAGCCAGAA ATCCAGTACG CACCACATTT GGAGCAGGAG CCTACAAATT 600
TGAGAGAATC ATCTCTAAGC AAAATGTCCT CAGATCTGCA AATGAGAAAT TCACAAGCGC 660
ACAGGAATTT TCTTGAAGAT GGAGAAAGTG ATGGCTTTTT AAGATGCCTC TCTCTTAACT 720
CTGGGTGGAT TTAACTACA ACTCTTGTC TCTCGGTGAT GGTATTGCTT TGGATTTGTT 780
GTGCAACTGT TGCTACAGCT GTGGAGCAGT ATGTTCCCTC TGAGAAGCTG AGTATCTATG 840
GTGACTTGGA GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTTGTTG 900
TTGTTAGATC TAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC 960
TTGCTCATTC TGAAATTTAA GCATTTTTCT TTTAAAAGAC AAGTGTAATA GACATCTAAA 1020
ATTCCACTCC TCATAGAGCT TTTAAAATGG TTTTATTGGA TATAGGCCTT AAGAAATCAC 1080
TATAAAATGC AAATAAAGTT ACTCAAATCT GTGAAGACTG TATTTGCTAT AACTTTATTG 1140
GTATTGTTTT TGTAAGTAATT TAAGAGGTGG ATGTTTGGA TTGTATTATT ATTTTACTAA 1200
TATCTGTAGC TATTTTGTTT TTTGCTTTGG TTATTGTTTT TTTCCCTTTT CTTAGCTATG 1260
AGCTGATCAT TGCTCCTTCT CACCTCTGC CATGATACTG TCAGTTACCT TAGTTAACAA 1320
GCTGAATATT TAGTAGAAAT GATGCTTCTG CTCAGGAATG GCCCACAAAT CTGTAATTTG 1380
AAATTTAGCA GGAAATGACC TTTAATGACA CTACATTTTC AGGAACTGAA ATCATTAAAA 1440
TTTTATTGTA ATAATTAATA AAAAAAAAAA AA 1472

```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
 1             5             10             15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
      20             25             30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
      35             40             45

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
      50             55             60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
      65             70             75             80

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
      85             90             95

```

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
 100 105 110
 Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
 115 120 125
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
 130 135 140
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
 145 150 155 160
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
 165 170 175
 Ile Val Ile Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
 180 185 190
 Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser
 195 200 205
 Ser Asp Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu
 210 215 220
 Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly
 225 230 235 240
 Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp
 245 250 255
 Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro Ser
 260 265 270
 Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu Gln Lys
 275 280 285
 Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg Ser Lys Thr
 290 295 300
 Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys Val Asn Leu Ala
 305 310 315 320
 His Ser Glu Ile

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GTGATTGGTA CAGTAGGTTT ATAAACAGAA GTTTAAACTT GTAAGCTTAA GCTTCCGTTT	60
ATAAACAGAA GTTTAAAATT ATAGGTCCTG TTAAACATTC AGCTCTGTTA ACTCACTCAT	120

Cys Ala Ala Gln Asn Ala Ser Leu Leu Lys Ile Asn Asn Lys Asn Ala
 165 170 175
 Leu Glu Phe Ile Lys Ser Gln Ser Arg Ser Tyr Asp Tyr Trp Leu Gly
 180 185 190
 Leu Ser Pro Glu Glu Asp Ser Thr Arg Gly Met Arg Val Asp Asn Ile
 195 200 205
 Ile His Ser Ser Ala Trp Val Ile Arg Asn Ala Pro Asp Leu Asn Asn
 210 215 220
 Met Tyr Cys Gly Tyr Ile Asn Arg Leu Tyr Val Gln Tyr Tyr His Cys
 225 230 235 240
 Thr Tyr Lys Gln Arg Met Ile Cys Glu Lys Met Ala Asn Pro Val Gln
 245 250 255
 Leu Gly Ser Thr Tyr Phe Arg Glu Ala
 260 265

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAGTTATATG	ACACTCAAAG	GAAAAGCAAA	AGAGCATTAA	GAAGTGTCTG	TTTTTGTTAT	60
TGCCATTTCA	TAAATATTTT	AGTAGGTGTT	CAATTTTCATT	GGATATTCTT	TTTTTTTAAT	120
TGTCTTTGTA	CCTATGATTG	AAAACAGTAG	TTGGTCTATG	ACTTTTGAGG	AGAGGGAGAA	180
CCGAAGATTA	CAGGAGGCCA	GCATGAGGTT	GGAACAAGAG	AATGATGACC	TTGCCCATGA	240
ACTAGTAACA	AGCAAAATTG	CTCTACGGAA	TGACTTGGAT	CAGGCAGAAG	ACAAGGCAGA	300
TGTGTTGAAT	AAAGAGCTCC	TTTTGACCAA	ACAGAGGCTG	GTGGAGACTG	AAGAGGAGAA	360
GAGGAAGCAA	GAGGAAGAGA	CTGCCCAGCT	AAAAGAAGTC	TTCAGGAAAC	AGCTAGAGAA	420
GGCAGAATAT	GAAATAAAGA	AGACTACAGC	TATCATTGCT	GAGTATAAAC	AGGTAATGTA	480
CTTCTGTGGC	ACATAGAGCT	AGTTATAGTT	TGCTGCTATA	AAAGTAATTT	TTTTTTTTTT	540
TTGCTTGAGG	CCAGGAGTTT	GAGACTAGCC	TGAGCAACAT	AGCAGGACTC	CGTCCCAAGG	600
AAAAAAAAAA	AAAAAAAAAA					618

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Ile	Glu	Asn	Ser	Ser	Trp	Ser	Met	Thr	Phe	Glu	Glu	Arg	Glu	Asn
1			5					10						15	
Arg	Arg	Leu	Gln	Glu	Ala	Ser	Met	Arg	Leu	Glu	Gln	Glu	Asn	Asp	Asp
		20					25						30		
Leu	Ala	His	Glu	Leu	Val	Thr	Ser	Lys	Ile	Ala	Leu	Arg	Asn	Asp	Leu
		35					40						45		
Asp	Gln	Ala	Glu	Asp	Lys	Ala	Asp	Val	Leu	Asn	Lys	Glu	Leu	Leu	Leu
	50				55					60					
Thr	Lys	Gln	Arg	Leu	Val	Glu	Thr	Glu	Glu	Glu	Lys	Arg	Lys	Gln	Glu
65				70				75						80	
Glu	Glu	Thr	Ala	Gln	Leu	Lys	Glu	Val	Phe	Arg	Lys	Gln	Leu	Glu	Lys
				85				90						95	

Ala Glu Tyr Glu Ile Lys Lys Thr Thr Ala Ile Ile Ala Glu Tyr Lys
100 105 110
Gln Val Met Tyr Phe Cys Gly Thr
115 120

- (2) INFORMATION FOR SEQ ID NO:191:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGCAGAATCC	AGAATGGATG	TCCTCTTTGT	AGCCATCTTT	GCTGTGCCAC	TTATCCTGGG	60
ACAAGAATAT	GAGGATGAAG	AAAGACTGGG	AGAGGATGAA	TATTATCAGG	TGGTCTATTA	120
TTATACAGTC	ACCCCCAGTT	ATGATGACTT	TAGTGCAGAT	TTCACCATTG	ATTACTCCAT	180
ATTTGAGTCA	GAGGACAGGC	TGAACAGGTT	GGATAAGGAC	ATAACAGAAG	CAATAGAGAC	240
TACCATTAGT	CTTGAAACAG	CACGTGCAGA	CCATCCGAAG	CCTGTAAC TG	TGAAACCAGT	300
AACAACGGAA	CCTAGTCCAG	ATCTGAACGA	TGCCGTGTCC	AGTTTGCGAA	GTCCTATTCC	360
CCTCCTCCTG	TGCTGTGCCCT	TTGTTTCAGGT	GGGGATGTAT	TTCATGTAGA	AGGTGGAAGA	420
AGGCTGCTAT	GACTCTTTGG	ATGGGAGTCT	GGCAAGAGGA	AATTGGAAGA	TAAAATAAAT	480
AATAAGTGAA	ATAAAAAAAAA	AAAAAAAAAA				510

- (2) INFORMATION FOR SEQ ID NO:192:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met	Asp	Val	Leu	Phe	Val	Ala	Ile	Phe	Ala	Val	Pro	Leu	Ile	Leu	Gly
1			5						10				15		
Gln	Glu	Tyr	Glu	Asp	Glu	Glu	Arg	Leu	Gly	Glu	Asp	Glu	Tyr	Gln	
			20					25				30			
Val	Val	Tyr	Tyr	Tyr	Thr	Val	Thr	Pro	Ser	Tyr	Asp	Asp	Phe	Ser	Ala
			35				40					45			
Asp	Phe	Thr	Ile	Asp	Tyr	Ser	Ile	Phe	Glu	Ser	Glu	Asp	Arg	Leu	Asn
	50					55			60						
Arg	Leu	Asp	Lys	Asp	Ile	Thr	Glu	Ala	Ile	Glu	Thr	Thr	Ile	Ser	Leu
65					70				75					80	
Glu	Thr	Ala	Arg	Ala	Asp	His	Pro	Lys	Pro	Val	Thr	Val	Lys	Pro	Val
				85					90				95		
Thr	Thr	Glu	Pro	Ser	Pro	Asp	Leu	Asn	Asp	Ala	Val	Ser	Ser	Leu	Arg
			100				105					110			
Ser	Pro	Ile	Pro	Leu	Leu	Leu	Ser	Cys	Ala	Phe	Val	Gln	Val	Gly	Met
		115					120					125			
Tyr	Phe	Met													
		130													

- (2) INFORMATION FOR SEQ ID NO:193:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

CATCTGACCA TCCATATCCA ATGTTCTCAT TTAAACATTA CCCAGCATCA TTGTTTATAA      60
TCAGAAACTC TGGTCCTTCT GTCTGGTGGC ACTTAGAGTC TTTTGTGCCA TAATGCAGCA      120
GTATGGAGGG AGGATTTTAT GGAGAAATGG GGATAGTCTT CATGACCACA AATAAATAAA      180
GGAAACTAA GCTGCATTGT GGGTTTTGAA AAGGTTATTA TACTTCTTAA CAATTCCTTT      240
TTTCAGGGAC TTTTCTAGCT GTATGACTGT TACTTGACCT TCTTTGAAAA GCATTCCCAA      300
AATGCTCTAT TTTAGATAGA TTAACATTAA CCAACATAAT TTTTTTTAGA TCGAGTCAGC      360
ATAAATTTCT AAGTCAGCCT CTAGTCGTGG TTCATCTCTT TCACCTGCAT TTTATTTGGT      420
GTTTGTCTGA AGAAAGGAAA GAGGAAAGCA AATACGAATT GTACTATTTG TACCAAATCT      480
TTGGGATTCA TTGGCAAATA ATTTTCAGTG GGTGTATTAT TAAATAGAAA AAAAAAATTT      540
TGTTTCCTAG GTTGAAGGTC TAATTGATAC GTTTGACTTA TGATGACCAT TTATGCACTT      600
TCAAATGAAT TTGCTTTCAA AATAAATGAA GAGCAGCTGT CCTTCTTCC TCTTTTAAGT      660
GTTTCAGCTGT GGCATGCTCA GAGGTTCCCTG CTGGATTCCA GCTGGAGCGG TGTGATACCC      720
TTCTTTTCA GCTGTTTCGTG CCTTCCTTTC TTGTATCCAC CAAAGTGGAG ACAAATACAT      780
GATCTCAAAG ATACACAGTA CCTACTTAAT TCCAGCTGAT GGGAGACCAA AGAATTTGCA      840
AGTGGATGGT TTGGTATCAC TGTAAATAAA AAGAGGGCCT GGG                        883

```

- (2) INFORMATION FOR SEQ ID NO:194:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Met Met Thr Ile Tyr Ala Leu Ser Asn Glu Phe Ala Phe Lys Ile Asn
1           5           10           15
Glu Glu Gln Leu Ser Phe Phe Pro Leu Ser Val Gln Leu Trp His
20           25           30
Ala Gln Arg Phe Leu Leu Asp Ser Ser Trp Ser Gly Val Ile Pro Phe
35           40           45
Phe Phe Ser Cys Ser Cys Leu Pro Phe Leu Tyr Pro Pro Lys Trp Arg
50           55           60
Gln Ile His Asp Leu Lys Asp Thr Gln Tyr Leu Leu Asn Ser Ser
65           70           75

```

- (2) INFORMATION FOR SEQ ID NO:195:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      110

```

- (2) INFORMATION FOR SEQ ID NO:196:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

TAGGCCTCTT TGGCCGGTGC TGCCTGAGAA GGATTGGCAC GGGCACAGAC CACTGCCCCC      60
ACCTGCCCTG CGCCATCTAC CCAAGAAGGC TCGGCACGGG CACCAACCAC TGCCTCCAAC      120
TGCCCCATGC TGCCTGAGAA GGCCTGCAC GGCCACCCCC AACTGCCCCG CACTGTCCCT      180
ACCCGGGCAG CCATGCGAGC GGCTGGAAC CTGCTGGCCT TCTGCTGCCT GGTCTTGAGC      240
ACCACTGGGG GCCCTTCCCC AGATACTTGT TCCCAGGACC TTAACACACG TGTGAAGCCA      300
GGATTTCCCTA AAACAATAAA GACCAATGAC CCAGGAGTCC TCCAAGCAGC CAGATACAGT      360
GTTGAAAAGT TCAACAAGT CACGAACGAC ATGTTCTTGT TCAAGGAGTC CCGCATCACA      420
AGGGCCCTAG TTCAGATAGT GAAAGGCCCTG AAATATATGC TCGARGTGGA AATTGGCAGA      480
ACTACCTGCA AGAAAAACCA GCACCTGCGT CTGGATGACT GTGACTTCCA AACCAACCAC      540
ACCTTGAAGC AGACTCTGAG CTGCTACTCT GAAGTCTGGG TCGTGCCCTG GCTCCAGCAC      600
TTCGAGGTGC CTGTTCTCCG TTGTCACTGA CCCCCGCCTC TTCAGCAAGA CCACAGCCAT      660
GACAAACACC AGGATGCATG CTCCTTGTC CCTCCCACCC GCYWSRTGAC CCRRCCTSAC      720
AGACCCTCTC RGGCCTCWGA CGAGTGAGCG GRTGAAGTGC MAYTGGGTSA CMGCAGGGCA      780
GCTRGAATGG CAGCWTGGTA GCGCTCCTA ACAGRTTAAA TRGATCACAT GTGMTTCTAA      840
AATTAAAAA AAAAAAAAAA A                                     861

```

- (2) INFORMATION FOR SEQ ID NO:197:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Met Leu Pro Glu Lys Ala Leu His Gly His Pro Gln Leu Pro Arg Thr
1.          5          10          15
Val Pro Thr Arg Ala Ala Met Arg Ala Ala Gly Thr Leu Leu Ala Phe
20          25          30
Cys Cys Leu Val Leu Ser Thr Thr Gly Gly Pro Ser Pro Asp Thr Cys
35          40          45
Ser Gln Asp Leu Asn Ser Arg Val Lys Pro Gly Phe Pro Lys Thr Ile
50          55          60
Lys Thr Asn Asp Pro Gly Val Leu Gln Ala Ala Arg Tyr Ser Val Glu
65          70          75          80
Lys Phe Asn Asn Cys Thr Asn Asp Met Phe Leu Phe Lys Glu Ser Arg
85          90          95
Ile Thr Arg Ala Leu Val Gln Ile Val Lys Gly Leu Lys Tyr Met Leu
100         105         110
Glu Val Glu Ile Gly Arg Thr Thr Cys Lys Lys Asn Gln His Leu Arg
115         120         125
Leu Asp Asp Cys Asp Phe Gln Thr Asn His Thr Leu Lys Gln Thr Leu
130         135         140
Ser Cys Tyr Ser Glu Val Trp Val Val Pro Trp Leu Gln His Phe Glu
145         150         155         160
Val Pro Val Leu Arg Cys His
165

```

- (2) INFORMATION FOR SEQ ID NO:198:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs

- (2) INFORMATION FOR SEQ ID NO:203:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TNACCTGCAT TTTATTTGGT GTTTGTCTG

29

- (2) INFORMATION FOR SEQ ID NO:204:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TNAACACTGT ATCTGGCTGC TTGGAGGAC

29

- (2) INFORMATION FOR SEQ ID NO:205:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GCAAGATTTG GCCTGGATTC TTCTGAGGAT GTGAAGTAAT GGAAACAGTA AGACTGTTCC	60
AGACTAGGGG AAGACTAGAG ACCTAATAGC TGGATTCCAT GTGATCTTTT GTTGGACTTT	120
GGGATTGGAG GTGAGAGTAG AGAAGGCATA ATGCACGTTT TTGAGACGAG GGAAATGTGA	180
ATATAGCCTG TATGCCTACA CTCAAGTCTG AAGACATGTW AACCATGTCT ATACTAACCA	240
GCCAAATATT TGAACACTAA AAGGAAGAAT TTTCTTAATG TGGTAATGGT WTCATGGTTG	300
TATAGAATGT TCCTCCTCTT GGGAGATGTG TGTTGAAAAT AGGGTTTGAC GTCTAAACCT	360
ATTTTGT TTTT GGCAAAAAGG ACGTGTGTCT GTACAAAAGA AGTGGAGCCA GTATGGCAAA	420
ATGTTTACMA GGA CTCTGGG TGAGARGTWC ATAGGTGCTT ACTATACTGT TTTGTTTCTG	480
AATTTGGAAT TTCTCAAAAT TAAAAAATA TCTACTGAGG AGCTTTTCGT TTTAACTGGT	540
GGGGAATGGG TTCTGGGTGG TTTTGCCCCCT TTTCTTTTTA GATTCAAGAA ATCCATGGTG	600

AAAGGTTTGG	ATTCCTATGA	AGAAAAGGAG	GATAAAGTGA	TCAAGGAGAT	GGCAGCTCAG	660
ATCCGTGAGG	TGGAGCAGAG	CCGACAGGAG	GTGGTTCGGT	CTGTCTTAGA	GGTTGGTTTC	720
CCTCGGAGGA	TCCAGACCAC	CTCAGGCAGT	GCCAGACCCA	GAAGAGGGCT	CTTCAGCACC	780
TAGAAGCTGG	AAAGGGATGA	ACAGGTAAGA	CTATTAGGGA	ATCTCTTGTT	GGGAATTTGA	840
CATCTTAGAA	CATTCTGCAA	CCTTTTGCCT	GGGAAATGGA	AACAGATCTA	ATCTTTACCA	900
CCCTCATGGC	TCAAGGACCT	CATCTGGCAG	CCTGGCTCAT	GTTTTTCAGC	CAAGTAGCTT	960
CCAGCTTACA	GCAGCCCTCA	AATTTGGACC	TGCCACCAGC	TCCAGAGCTT	GACTGGATGG	1020
AGACAGGACC	ATCTCTGACA	TTCATTGGCC	ATCAGGTACA	AAGGATAAGC	AAGCCAGAAG	1080
AGGGCCAATG	GTCCCTCAGG	TCTCAGGACC	CCTTTCTCCT	GATTTTCTAC	CTATTCAAGC	1140
CACTGCTGCC	TCCACTGCAG	GCTTTTCCTT	CTTCCTTCAC	TGTTCCCTAG	TAGTGTTCTC	1200
AGACCTCTTC	TCACCCTCCA	AAGCGATCCT	ATTACATGT	ATTGACACTT	AGGAGTGCCA	1260
ACTCCTAAAT	CTTGCCCTCT	GTAAGACTCA	TAGTTCCAAC	TCAACACAGG	ACATTAAATA	1320
TCCCACAGGC	ATCTGAAACT	AACCCCCACC	ACTCCTATAT	TTCCAATCAC	TAGATGCAGA	1380
TCCTTTCTCT	TTCCATCTCC	CATATCCTGT	CAACAAGCGG	TCAATTTTAA	CCTGTCTGCC	1440
TCCATTCAGC	CTTTGGGCAA	TTTCTACTCC	CCCTTCAATC	CTGCCTCACA	AACAGAAAAT	1500
CATTGTACCA	CTTATGATTT	TACTCTACAC	TTCAGCTGTA	TTGTGTTGCT	TCGGGCTTTT	1560
GCAGTTGCCA	TTGTCTAAAA	CATGCTTTCC	TTCCCTCATC	ACCTAGTTTA	CCTTCAACTG	1620
TTAGCTCAAA	TGTCACCTTT	TCATAAAAGG	CTTATCTGAA	CAGGTTATCT	CTATTTCAAG	1680
TGGATGTAGC	ACCATGTAAA	GTTGCAAATG	TAATTTACGT	AACTTGTGCT	TAATGCTCTT	1740
CCCCAATTAT	ATGTATGCTG	TGAGGGCAAG	GTTTTGCTCC	CCTGGCATGT	AATAGCCACT	1800
CTACTTACAG	ACATCTCCAC	TGTTATGACT	GTGAGCTTCC	TGAGGACAGG	GTTGTCTTAG	1860
AGTGACTTAC	TGTGCTTTCA	AAGTTTAACA	TCAGCTGGGG	TGCAGAATTA	GCATTGTGGC	1920
AGCAGTCACA	CCCACCTCTT	TTAAAGTGTG	CTTTGTCTAT	CGTTTCTAGG	ATTTTTTTTT	1980
TTAATCATGC	CTAGACTTTA	ACTAGCACTT	TTTTTCCCAT	TTCCAACACT	AGGATATAACC	2040
AGGAGTTGGT	AACATCCACT	CAGGTGCCAC	ACCTCCCTGG	ATGATCCAAG	ATGAAGAATA	2100
CATTGCTGGG	AACCAAGAAA	TAGGACCATC	CTATGAAGAA	TTTCTTAAAG	AAAAGGAAAA	2160
ACAGAAGTTG	AAAAAACTCC	CCCCAGACCG	AGTTGGGGCC	AACTTTGATC	ACAGCTCCAG	2220
GACCAGTGCA	GGCTGGCTGC	CCTCTTTTGG	CCGTGTCTGG	AATAATGGAC	GCCGCTGGCA	2280

GTCCAGACAT CAATTCAAAA CTGAAGCTGC AGCAATGAAG AAGCAGTCAC ATACAGAAAA 2340
 AAGCTAATCA TGCTCTCTAC CAACTACCAT GAGGCTAAAA GCAAAGTCAA CAAACCCCTA 2400
 TTATACCTTC CACCAAATTC TTTATCAT TG TCTTTCTTAG GAAACAGACA TACTCATTCA 2460
 TTTGATTTAA TAAAGTTTAA TTTTCCAAA TGTACAGCTG GTTGGACCTG TAAAAAAAAA 2520
 TTAAAAGAAT CAGAACCATA AAAAAAAAAA AAAAAA 2556

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met	Glu	Thr	Asp	Leu	Ile	Phe	Thr	Thr	Leu	Met	Ala	Gln	Gly	Pro	His	1	5	10	15
Leu	Ala	Ala	Trp	Leu	Met	Phe	Phe	Ser	Gln	Val	Ala	Ser	Ser	Leu	Gln	20	25	30	
Gln	Pro	Ser	Asn	Leu	Asp	Leu	Pro	Pro	Ala	Pro	Glu	Leu	Asp	Trp	Met	35	40	45	
Glu	Thr	Gly	Pro	Ser	Leu	Thr	Phe	Ile	Gly	His	Gln	Val	Gln	Arg	Ile	50	55	60	
Ser	Lys	Pro	Glu	Glu	Gly	Gln	Trp	Ser	Leu	Arg	Ser	Gln	Asp	Pro	Phe	65	70	75	80
Leu	Leu	Ile	Phe	Tyr	Leu	Phe	Lys	Pro	Leu	Leu	Pro	Pro	Leu	Gln	Ala	85	90	95	
Phe	Pro	Ser	Ser	Phe	Thr	Val	Pro									100			

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TTCATCTTCT CCCTGTAAC T GAGATTTCTA CCACACCTTT GAACAATGTT CTTTCCCTTC	60
TGGTTATCTG AAGACTGTCC TGAAAGGAAG ACATAAGTGT TGTGATTAGT AGAAGCTTTC	120
TAGTAGACCA TATTTCTTCT GGATTGTAAT AAAATTGTGA GTAGCTCCTT TTA CTTTGT	180
CCTGTCTCTG GAAAGCCATT TTTGAATTGC TGATTACTTT GGCTTTAATC AGTGGTCACC	240
TAGAAAAAGC TTTGTAATCA TAACACAATG AGTAATTCTT GATAAAAAGTT CAGATACAAA	300
AGGAGCACTG TAAAACTGGT AGGAGCTATG GTTTAAGAGC ATTGGAAGTA GTTACAAC TC	360
AAGGATTTTG GTAGAAAGGT ATGAGTTTGG TCGAAAAATT AAAATAGTGG CAAAATAAGA	420
TTTAGTTGTG TTTTCTCAGA GCCGCCACAA GATTGAACAA AATGTTTTCT GTTTGGGCAT	480
CCTGAGGAAG TTGTATTAGC TGTTAATGCT CTGTGAGTTT AGAAAAAGTC TTGATAGTAA	540
ATCTAGTTTT TGACACAGTG CATGAAC TAA GTAGTTAAAT ATTTACATAT TCAGAAAGGA	600
ATAGTGGAAG AGGTATCTTG GTTATGACAA AGTCATTACA AATGTGACTA AGTCATTACA	660
AATGTGACTG AGTCATTACA GTGGACCCTC TGGGTGCATT GAAAAGAATC CGTTTTATAT	720
CCAGGTTTCA GAGGACCTGG AATAATAATA AGCTTTGGAT TTTGCATTCA GTGTAGTTGG	780
ATTTTGGGAC CTTGGCCTCA GTGTTATTTA CTGGGATTGG CATACGTGTT CACAGGCAGA	840
GTAGTTGATC TCACACAACG GGTGATCTCA CAAAAGTGGT AAGTTTCTTA TGCTCATGAG	900
CCCTCCCTTT TTTTTTTTAA TTTGGTGCCT GCAACTTTCT TAACAATGAT TCTACTTCCT	960
GGGCTATCAC ATTATAATGC TCTTGGCCTC TTTTTTGCTG CTGTTTTGCT ATTCTTAAAC	1020
TTAGGCCAAG TACCAATGTT GGCTGTTAGA AGGGATTCTG TTCATTCAAC ATGCAACTTT	1080
AGGGAATGGA AGTAAGTTCA TTTTAAAGTT GTGTTGTCAG TAGGTGCGGT GTCTAGGGTA	1140
GTGAATCCTG TAAGTTCAAA TTTATGATTA GGTGACGAGT TGACATTGAG ATTGTCCTTT	1200
TCCCTGATCA AAAAATGAAT AAAGCCTTTT TAAACAAAAA AAAAAAAAAA AAAAAAAAAA	1260
AAAAAAAAAA AAAAAA	1276

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Ile Leu Leu Pro Gly Leu Ser His Tyr Asn Ala Leu Gly Leu Phe
1 5 10 15
Phe Ala Ala Val Leu Leu Phe Leu Asn Leu Gly Gln Val Pro Met Leu
20 25 30
Ala Val Arg Arg Asp Ser Val His Ser Thr Cys Asn Phe Arg Glu Trp
35 40 45
Lys

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGGCTCGTC TGTTCCAGGA GCCCTGAACC AAAGAGCAGC GGAGTTTGAG AAGCCAGCAG 60
CTCGGGGTTC GGCAGCAGCG GTCCCATCGG CTGAAGTTTC GGGGGGGTGG GGCGCCGAGC 120
GCGCGGGGTG GGGGGGGTCC TGGTCTTTGG CTTCTCGACT CGGTCCTGTT TCGACAGCGA 180
ACATGTCGCG GCCTGTCAGA AATAGGAAGG TTGTTGATTA CTCACAGTTT CAGGAATCTG 240
ATGATGCAGA TGAAGATTAT GGAAGAGATT CGGGCCCTCC CACTAAGAAA ATTCGATCAT 300
CTCCCCGAGA AGCTAAAAAT AAGAGGCGAT CTGGAAAGAA TTCACAGGAA GATAGTGAGG 360
ACTCAGAAGA CAAAGATGTG AAGACCAAGA AGGATGATTC TCACTCAGCA GAGGATAGTG 420
AAGATGAAAA AGAAGATCAT AAAAATGTGC GCCAACAACG GCAGGCGGCA TCTAAAGCAG 480
CTTCTAAACA GAGAGAGATG CTCATGGAAG ATGTGGGCAG TGAGGAAGAA CAAGAAGAGG 540
AGGATGAGGC ACCATTCCAG GAGAAAGATT CCGGCAGCGA TGAAGATTTC CTAATGGAAG 600
ATGATGACGA TAGTGACTAT GGCAGTTCGA AAAAGAAAAA CAAAAGATG GTTAAGAAGT 660
CCAAACCTGA AAGAAAAGAA AAGAAAATGC CCAAACCCAG ACTAAAGGCT ACAGTGACGC 720

CAAGTCCAGT GAAAGGCAAA GGGAAAGTGG GTCGCCCCAC AGCTTCAAAG GCATCAAAGG 780
AAAAGACTCC TTCTCCCAAA GAAGAAGATG AGGAACCGGA AAGCCCGCCA GAAAAGAAAA 840
CATCTACAAG CCCCCCACCC GAGAAATCTG GGGATGAAGG GTCTGAAGAT GAAGCCCCTT. 900
CTGGGGAGGA TAAAAGTGA TGATGGTCTG GGGAGAGATT TTATTAAAAA AAAAAAGAAA 960
AAAAAAGAAA AAAGAGGGAG GAAAAAAG AACCTACTTA AGATAGAACA TGGTTTTGGC 1020
TATGGCTTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080
AAAAAAAAAA AAAAAAAAAA AAAAAAAA 1108

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met	Ser	Arg	Pro	Val	Arg	Asn	Arg	Lys	Val	Val	Asp	Tyr	Ser	Gln	Phe	
1				5					10					15		
Gln	Glu	Ser	Asp	Asp	Ala	Asp	Glu	Asp	Tyr	Gly	Arg	Asp	Ser	Gly	Pro	
			20					25					30			
Pro	Thr	Lys	Lys	Ile	Arg	Ser	Ser	Pro	Arg	Glu	Ala	Lys	Asn	Lys	Arg	
			35				40					45				
Arg	Ser	Gly	Lys	Asn	Ser	Gln	Glu	Asp	Ser	Glu	Asp	Ser	Glu	Asp	Lys	
			50			55				60						
Asp	Val	Lys	Thr	Lys	Lys	Asp	Asp	Ser	His	Ser	Ala	Glu	Asp	Ser	Glu	
65					70					75					80	
Asp	Glu	Lys	Glu	Asp	His	Lys	Asn	Val	Arg	Gln	Gln	Arg	Gln	Ala	Ala	
				85					90					95		
Ser	Lys	Ala	Ala	Ser	Lys	Gln	Arg	Glu	Met	Leu	Met	Glu	Asp	Val	Gly	
			100					105					110			
Ser	Glu	Glu	Glu	Gln	Glu	Glu	Glu	Asp	Glu	Ala	Pro	Phe	Gln	Glu	Lys	
			115				120					125				
Asp	Ser	Gly	Ser	Asp	Glu	Asp	Phe	Leu	Met	Glu	Asp	Asp	Asp	Asp	Ser	
			130			135					140					
Asp	Tyr	Gly	Ser	Ser	Lys	Lys	Lys	Asn	Lys	Lys	Met	Val	Lys	Lys	Ser	

145 150 155 160
 Lys Pro Glu Arg Lys Glu Lys Lys Met Pro Lys Pro Arg Leu Lys Ala
 165 170 175
 Thr Val Thr Pro Ser Pro Val Lys Gly Lys Gly Lys Val Gly Arg Pro
 180 185 190
 Thr Ala Ser Lys Ala Ser Lys Glu Lys Thr Pro Ser Pro Lys Glu Glu
 195 200 205
 Asp Glu Glu Pro Glu Ser Pro Pro Glu Lys Lys Thr Ser Thr Ser Pro
 210 215 220
 Pro Pro Glu Lys Ser Gly Asp Glu Gly Ser Glu Asp Glu Ala Pro Ser
 225 230 235 240
 Gly Glu Asp

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2952 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ASTTCRAATT CGGCCTTCAT GGMCTAGCAC GGACTCTGCC TTCTAAAAGT GGAACCCCMC	60
AGTMCCAGCT GTTGCCTMAG SGTGGACASA TCAGSCGAAG CTCCTGCCCT GCCTGTTGGC	120
AGCMTCCATG GGCCAAGCTC TTGCCTCTCA CCATCCTCTC CAGGCCCAGT ACTGTTTCCA	180
GCCGGCCTCT CCAGGCCCAA CTCTCCCTCT CAGCTGTGCC TGCCGGCCCA GCTCCTACCT	240
CGCAAAAGCC ACGTTCGGCC CAGCTCCTGC CCAGCTCCTG GCAGCCTTTG TAAACCCAG	300
GATCCTCTAA GTCAGGCCTT TCAGGCCCTG CCTTTGGCTC CCCGGTGGCA TGGAGAGGCC	360
CAGCTCCTGC CTGACAGCGG CCTCTCCAGG CCCAGCTCTT GCCTCACGTT GGCCTCCCTG	420
GGCCACGTTT CCGCCTGCCT CGCGGCAGCC CCGACAATCC CGGCTCCTGC CTCCCGATGG	480
CATCTTTAGG CTCATCTCGT GCCTCACCAC GGCCTGCACC AGGCCACACT CCTGCCTTTC	540
GGTGGCCTCC GCGGGCCTGA CTCCTGCGTC CCAATGGCCT CTTTAGGCCC GGCTCGTGCC	600
TCGCCGCGGC CTCCTGAGGC CCACCTTTGC CTTTCTGGCA GCCTCTCCAG GCCCAGGACT	660
TCCTCAAGTC GGCCTCTGCC AGCCCAGTGG CCGCCTCCCG GCCTCCTCTC CGGGCCCAGC	720

TCCTTGCTCG	TGGCTGCGCC	CGCGGGCCCCA	GCTCCTGCCT	CTGAACATCC	TCCTGTGACT	780
CGGCTCCTGC	CCAGCTCCCA	GCGGCCTCCG	TAGACCCGAA	GCCTCCTCCG	GTCCAGCTCT	840
CCAGGCCTGC	CTCCTGCCTC	GTGGCGGCCT	TCCCCGGCCA	TGCTCGTGCC	GGCTTCCCGG	900
CAGCCTCCAC	GAGCCCGGCT	CCTGCCTCAC	GCGGGCCCCCT	CCAGGCCCCAG	CTCGTGCCTC	960
GCGGCGGCCT	CTCCAGGCCC	GGCTCCCGCC	CAGCCCGACG	GCGTCTCCCA	GCCCAAGGCT	1020
CCCTTCCTCA	ACGTCGGCCC	CTCTGGGCCC	AGCTCCTGCC	TCCCGCTGAT	GGCCTGTGCG	1080
GGCCACCCG	AGGCGGCCCCG	AAGTCGGCCT	CGCCAGGCCC	AGCTCCTGCC	TGGCGTAGGC	1140
CCCTGGGGGC	ACGGCCTCTG	CCCMACAGTG	GCCCCCTCCGG	GCCCAGCTCG	TGCCTCGGCT	1200
TGGCCGCCTC	AGGCCCAGCT	CCTGCCTGTG	GGCGGCCTCT	CTCCAGACCC	GGCTCTCGCC	1260
TCCCGGCATC	CTCTCCAGGC	CCAGAGCTGT	TTCCAGTTGC	TAGACCATTT	TTGTGCCTGC	1320
CTCGTTGCAG	CATCTCCAAG	CCCAGCTTTT	GCTTTTCTGC	AGTTTCTTGA	GGCCGAACTC	1380
CATTTTTCGA	ATGGCTTATT	TAGGCCCAGC	TCTTGCGTTT	GCATTGTCCC	TTCAGGCCCCA	1440
GAACTTTCTC	ACGTCATCGT	CACCAGGCCT	AGCTTCTGCA	TCTGGTCAGC	CTTTTAAGGC	1500
CCAGCTTTTG	CCTCATAAAC	TCAGCTCCTG	TTTAATGGCG	GCCTCCAGG	TCCCACCTTC	1560
TGCCTTCCTG	TGTCCACTCC	AGGCCCAGCT	ACTGCCTTGG	TGCTCTTTTT	AAGTCAATAA	1620
TTTTTTCCAG	TCGACCTCTC	CAGGCCCCAAC	TTGTACCTCT	GAGTGTCCTC	TAGGATCTCA	1680
GCTTCTGCCT	AACAATGACC	TCTTTAGACT	CAGCTCATTT	TCACTGCTAC	ATCTTCAAGC	1740
CATTCTCCTG	CCTCTTGGA	ACCTCTAGTG	GCCCAGCTTC	TGCCTCACAG	CAGCCTCTCC	1800
ATGCATGCCT	AGCTCCTGCC	TCTTTAGGGA	ACTTACAGGC	CTAAAACTTT	CTTAATTTGG	1860
GCTTCTCAAG	CCCAGCTCCT	GCCTTCTGTT	GGGCTCTACA	GGCCTGGCAT	CATCCTTTCA	1920
ACAGCCTCTT	TAGGCCCCGGC	CTCTCCAGGA	CCAAAACATC	CTTAAGTCAA	CCTCACCAGG	1980
CCCGGCTCCT	GTCTCCTTGC	GGCCTCCAGA	GGCCGAGCTT	TTGCCTGCCA	ATGGCCTCTC	2040
TAGCCCCAGC	TTTTGCCTGC	CAATGGCCTC	TCTAGCCCCA	GCTTCTGCCT	TTCATCGGTC	2100
TCTCCAGGCT	TAGCTCCTTT	CTCTTCACGG	CCTCTGCAGG	CCTAAAACTT	CCTCAATTTG	2160
GCATCTCCAG	GCCCAGCTCC	TGCCTCCAGG	CCGCCTCTGC	AGGCCTATCT	CAAGCCTTAC	2220
AACAGCCTCT	TTACCCCCAG	CTCCTTTCTC	CGACTTGTCT	CTCCAGGCCT	AGAACTTCCT	2280
CATGTTTACC	TCACCAGGCC	CACCTCCTGC	CTTCCAGTAG	CGTCTACAAG	TTTGGCTCCT	2340
GCCTCCCATG	GATCTCTCCA	GGCCCCAAAC	TTTCTCAAGT	CAACCTCACC	AGGCCCGGCT	2400
TCTCCCTTTC	ATCAGCCTTC	CAAAGGCCAG	CTTTTGCTTC	ATGTCTGCCT	TCCGAGTCCC	2460

AGCTCCTGTT TTATGGCAGC CTCCTGAGGC CCAGCTCCTG CCTCCTAGTG GCCTCTTTTG 2520
 GCCCAACTCT TTCCTCACCA GGGCCTTCCA GACCACGTTT CTGCCTTTTA GCAGCCACTA 2580
 CAGGCCCAGC TTTGCGTCCT TTCAAGAGTC CTGCCTCACA GTGGCCTCCC AAGGGCAACT 2640
 TTCTGCCTCA TGTCAGCCTC TTGTGCCCTG GTCCTGCTTC CTGGTAGACT CTGCAGGCCC 2700
 TGCTCCTGCC TTACGTTGCC CCTTTTATAA AGATCCAGTT CCTGCCTCCT GGCTGCCTCT 2760
 ATGAGCCCAA ATCCTGCCTA ACAACAACCT GTTTTTGCCC AGCTCCTGCT TCCTGGCAGC 2820
 CTCCTTAGGC CAAAATTTC CTTCAGTTGA CCTCTCCAGG CCCAGCTCCT GCCTCTCAGC 2880
 ACCCTCTTTA GGCCCAGCTC CTGCCTTAAT AAATTGAAT AAATTATTGT TATGTGAAAA 2940
 AAAAAAAAAA AA 2952

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met Ala Tyr Leu Gly Pro Ala Leu Ala Phe Ala Leu Ser Leu Gln Ala
 1 5 10 15
 Gln Asn Phe Leu Thr Ser Ser Ser Pro Gly Leu Ala Ser Ala Ser Gly
 20 25 30
 Gln Pro Phe Lys Ala Gln Leu Leu Pro His Lys Leu Ser Ser Cys Leu
 35 40 45
 Met Ala Ala Ser Gln Val Pro Pro Ser Ala Phe Leu Cys Pro Leu Gln
 50 55 60
 Ala Gln Leu Leu Pro Trp Cys Ser Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GTGCCCCGCC GCTGCTGTCA CCCCCGGCCG CTGCTGCCCT CCCC GCCGAG GTTCTACTGC	60
TCTCCTTCTT AAGAAGGGTG GGAGGCACTC GGTCTCTCCC CACACCTCTC GCCTGAGGCC	120
AGGCGCCAGG TGTCGCCTGA AGCCAGACAG CCGGTTTGGG AGCGAGCCTG AGGTCAACCA	180
ATCAATGGCT CAGACAGATA AGCCAACATG CATCCC GCCG GAGCTGCCGA AAATGCTGAA	240
GGAGTTTGCC AAAGCCGCCA TTCGGGCGCA GCCGCAGGAC CTCATCCAGT GGGGGGCCGA	300
TTATTTTGAG GCCCTGTCCC GTGGAGAGAC GCCTCCGGTG AGAGAGCGGT CTGAGCGAGT	360
CGCTTTGTGT AACTGGGCAG AGCTAACACC TGAGCTGTTA AAGATCCTGC ATTCTCAGGT	420
TGCTGGCAGA CTGATCATCC GTGCAGAGGA GCTGGCCCAG ATGTGGAAAAG TGGTGAATCT	480
CCCAACAGAT CTGTTTAATA GTGTGATGAA TGTGGGTCGC TTCACGGAGG AGATCGAGTG	540
GCTGAAGTTT TTAGCCCTTG CTTGCAGCGC TCTGGGAGTT GTAAGTTAGC TTGACTGTTT	600
TTTGTTCCTG AAGGGGAAAT CTCCCTCTGG GCCTGGAAGG GCAGTGCATC TATACACGCG	660
GTCAACTCTG CAGGGCTGAT GATAAACATG CCTCTTCTCC TATTGTCCTT CTCCTCTCTA	720
AAGCAAGGTC ATTTCTGTGC TCGTCAGGCA GTGGCAGGGG TTGGGAGGAG GAGAGAGGGA	780
AACACTGTGG TCAGGCTCTG GGGAGAGTTG ACTACAGTGT AGCTCTTGGA TTATTTATGA	840
ATATTGCCCT CAGATTTATT TTTACTCTGC TCCTTCCATT CATATTCCCA GAGACAACCA	900
AGAGCCGACT GTAGAAAAG ACTTCCAGAC ACCTAGAATA TATATCAATA GACACTGTTT	960
AAAAGGGGTA CAATCTTATA GAAAACATG TAATAAACAG AATTGGATGC AGAACTCAGA	1020
CATAAGAAAG CAAAAACAAA GAGAGATGAG GCTATTTCTG AATTAGTCA TGACATCTCC	1080
ATGGATACAG GATGTTTATA CAGATTTATG CCTTTTCCAA ATTTGACTTG TTTGATATTG	1140
GAAAAACAAT TTTACTGTTT TGAAGCCAAA GATGTTGAAA TCAGTTTATA TGTATAGATA	1200
TTTAAAGCTT GGGTATCTTA TATGTGGACT TACATTGTTA AACATTGTTA AAATAAAATG	1260
AATCAAAAAC ATGGTTTTTTA AAAAAAAAAA AAAA	1294

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Ala Gln Thr Asp Lys Pro Thr Cys Ile Pro Pro Glu Leu Pro Lys
1 5 10 15
Met Leu Lys Glu Phe Ala Lys Ala Ala Ile Arg Ala Gln Pro Gln Asp
20 25 30
Leu Ile Gln Trp Gly Ala Asp Tyr Phe Glu Ala Leu Ser Arg Gly Glu
35 40 45
Thr Pro Pro Val Arg Glu Arg Ser Glu Arg Val Ala Leu Cys Asn Trp
50 55 60
Ala Glu Leu Thr Pro Glu Leu Leu Lys Ile Leu His Ser Gln Val Ala
65 70 75 80
Gly Arg Leu Ile Ile Arg Ala Glu Glu Leu Ala Gln Met Trp Lys Val
85 90 95
Val Asn Leu Pro Thr Asp Leu Phe Asn Ser Val Met Asn Val Gly Arg
100 105 110
Phe Thr Glu Glu Ile Glu Trp Leu Lys Phe Leu Ala Leu Ala Cys Ser
115 120 125
Ala Leu Gly Val Val Ser
130

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TTTTTTTTTT TTTTGTATA GCAATGGAAG AATGGCCTCG TACACACGCT AGAGTGGAAA 60
GTCCCAGGCA CCAAGGCTTC CCACCCTAGA AGCAAGCTCA GGGCTTCTC TTCATCCTTC 120
CAGGGAGAGC ACTGAGAGAT GATGGGGGGT TGGCAGGGGG CATCCCTTGG ATTATCATTC 180
TCCAGACTTA GGCTTGGAGG GGAGGGTGA GAAGTGGATT TCTGGGTCTG GTCCACCTCA 240

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CCTGTTTTCT CAGCTTCTCA CCCACTCAGA GCTCTTGCCC CAATTCTCCC TTTCATCCTG      300
CAGATCCCTG CGCCTGACTC ATCTCAGGCG AGGAGGCAAA TCATCAGTTA TCTCAGGCAG      360
CAGCAGGACG AGACTCCTTT CTGATTTTCT CCTTCCCTGG CCACCTCTCC CCACCCCAT      420
TTCACTCATT CCAAACCTCT GGCTCCCCA GCAACTCTAC ATCCTCATCT CCACCTGTTC      480
CCTCTCTCGA TGCTGTGGGT GACGTTGGAG AGGGAAGCCC GGAGCCCTGA CCTAGTCCGG      540
CGTGGAGAGA GGAATGGAAA GCAGTGTCCT TTTTGAGAAG GCAAATTTAC AGCTGGCTTT      600
TGTAATCCTA GCTATTTTTT GTTTGTTTGC TAAGTCTTTG ATAGTCCCCA GTGTGGTTTG      660
TCTGCCAGTG ATCTCAGCAC CACCAGAGAG CTTGTTAGAA ATGCGGCATC CCAACCCAC      720
CACAGCCCTC CCAAGTCAGA TACTGCCACC TCACGAGGCC CCCCAGGGAT CCACAAGTTC      780
ATTAAAGTTT CAGGAATCCA ATTCTACTAC AAAATATACA TTTATAATTA GGAAAAGGAT      840
AGTTCTTTTA AATGGTAGAA CTTCCTCAAT GAGTCAGCTA CCTGTATTTT TGGCCTGTCA      900
GGCTAGACAC TGGAGACCAT TCTGCATAGA ATTGTACCTC CCTGAACTAC TGTTAGGCCT      960
TAGGGTGGGG ATTCATCTTT CCCTTCTCCC CACCATGGAG ACAAATCCT CTTAAACATA     1020
TCCGGGCCTG GCATGGTGGY TMACGCCTCG GCCTCCCAA GTTCTGGGAT TACAGGCATG     1080
AGCCAYTGTG CCCAGCCACC CGTCACCTGY TAGTGTAGAC AAATGAATAA ACTTAGACAA     1140
GCACATGGGC TCCCTCTATA CCAGCCTAGA CTTTGACACT GAAACTCCAT GAGTCTGGGC     1200
CACTTCCTGC CACAAGTGTG AATGGAAAAT AAATCATTTT CCAAGGAACC CAAAATCACT     1260
AAGCCAAGGA GTCAAGCTGA GAACTTTCAG GCAAACCTGC CCCCATTTT ATTTCTTAAA     1320
TAAGAGAGCT ACAAAGATTA AAAAAAAAAA AAAA                                1354

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(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

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Met Glu Ser Ser Val Pro Phe Glu Lys Ala Asn Leu Gln Leu Ala Phe
1           5           10          15
Val Ile Leu Ala Ile Phe Cys Leu Phe Ala Lys Ser Leu Ile Val Pro

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20	25	30
Ser Val Val Cys Leu Pro Val Ile Ser Ala Pro Pro Glu Ser Leu Leu		
35	40	45
Glu Met Arg His Pro Asn Pro Thr Thr Ala Leu Pro Ser Gln Ile Leu		
50	55	60
Pro Pro His Glu Ala Pro Gln Gly Ser Thr Ser Ser Leu Lys Phe Gln		
65	70	75
Glu Ser Asn Ser Thr Thr Lys Tyr Thr Phe Ile Ile Arg Lys Arg Ile		
85	90	95
Val Leu Leu Asn Gly Arg Thr Ser Pro Met Ser Gln Leu Pro Val Phe		
100	105	110
Leu Ala Cys Gln Ala Arg His Trp Arg Pro Phe Cys Ile Glu Leu Tyr		
115	120	125
Leu Pro Glu Leu Leu Leu Gly Leu Arg Val Gly Ile His Leu Ser Leu		
130	135	140
Leu Pro Thr Met Glu Thr Lys Ser Ser		
145	150	

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1628 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CCCCGGTCCC CGCCGAGCC GCTGCATCCT CCGTGCCCGG CCTGAGCTGG AGTCCCCCGC	60
GCCCCCGCG TTCCGCCCCG CCATGGCTGC GGTGGCGCTG ATGCCACCGC CGCTGCTGCT	120
GCTGCTGCTG TTGGCGTCGC CGCCCGCCGC CTCCGCGCCG TCCGCCCCGCG ATCCCTTCGC	180
CCCCCAGCTC GGGGACACGC AGAACTGCCA GCTGCGGTGC CGCGACCGCG ACCTCGGCCC	240
GCAGCCCTCG CAGGCGGGGC TGGAGGGCGC CTCCGAGTCT CCCTATGACA GAGCCGTTCT	300
GATCAGCGCT TGCGAGCGTG GCTGCCGCCT CTTCTCCATC TGCCGATTG TGGCCAGAAG	360
CTCCAAGCCC AATGCCACCC AAAGTGAGTG TGAAGCAGCC TCGGTGGAAG CCTATGTGAA	420
GGAGGCAGAR CAGCAGGCCT GTAGCCACGG CTGCTGGAGC CAGCCCGCGG AGCCTGAGCC	480

GGARCAGAAG AGAAAGGTCC TGGAGGCTCC AAGTGGGGCC CTCTCCCTCT TGGACTTGTT 540
 TTCCACCCTC TGCAATGACC TTGTCAACTC AGCCCAGGGA TTTGTCTCCT CCACCTGGAC 600
 ATACTACTTG CAGACTGACA ATGGGAAAAGT GGTGGTGT TT CAGACTCAGC CCATAGTGGA 660
 GAGCCTCGGC TTCCAGGGGG GCCGTCTGCA GCGCGTGGAG GTGACCTGGC GAGGCTCCCA 720
 CCCTGAAGCC CTGGAGGTGC ACGTGGACCC TGTAGGCCCC CTGGACAAGG TGAGGAAGGC 780
 CAAGATCCGA GTCAAGACCA GCAGCAAGGC CAAGGTGGAG TCTGAAGAGC CACAGGACAA 840
 TGA CTTCCTC AGTTGCATGT CCCGGCGCTC GGGTCTGCCT CGCTGGATCC TGGCCTGCTG 900
 CCTCTTCCTC TCCGTGCTGG TGATGCTGTG GCTGAGCTGC TCCACCCTGG TGACCGCGCC 960
 TGGCCAGCAC CTCAAGTTCC AGCCTCTGAC CCTGGAGCAG CACAAGGGCT TCATGATGGA 1020
 GCCCATTGG CCCCTGTACC CGCCGCCGTC CCACGCCTGT GAGGACAGCC TACCACCCTA 1080
 CAAGCTGAAG CTGGACCTGA CCAAGCTGTA GGCCTCCACT GGCCCCATCA CTGCCAACTG 1140
 CAGGGGGCCC CTCGGGCCTC ACTTGCCCTG AGCCCAGGAG TCCAAGGGCA GGGTGGGTCC 1200
 AGCGTTGAGC CCCTCCACCC CCAAATCCTT CCTCTCCTCC CAGTCCCACC CCTTGCCCCA 1260
 CGGAGTCCTG GGGACGCAGT GCCCCAGCTG GGAAGAGGGC GGGATCGGGC ACTGGTTCCT 1320
 CCTTGTCCTG GCTTTCTTGG GGGCTTGCTA CTTTTTGTCT TCTATTGTGT GGCTTTCTGA 1380
 GTATTTGAAC CCCAGTCCTG TGTCACCTTC CTTTTTCCTT CTATGTCCCC TCTCTGCGGG 1440
 GGGGGCGCTG AGGCTGAGGG GGAGCTGCGT CTTGCTAGGG CTTCCCCCTT CTCCCCATCC 1500
 CGGTCTCCAG AGACCCAGCT TCTGAGAGAC AGGGTGTGGG CATCTCCATG CCCCTATAAA 1560
 GCGTGCCTGG GGCTTGTCTG GGGCTGGGGA GGAATAAACC ATGTATATAA AAGAAAAAAA 1620
 AAAAAAAA 1628

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Ala Ala Val Ala Leu Met Pro Pro Pro Leu Leu Leu Leu Leu Leu
 1 5 10 15

Leu Ala Ser Pro Pro Ala Ala Ser Ala Pro Ser Ala Arg Asp Pro Phe
 20 25 30
 Ala Pro Gln Leu Gly Asp Thr Gln Asn Cys Gln Leu Arg Cys Arg Asp
 35 40 45
 Arg Asp Leu Gly Pro Gln Pro Ser Gln Ala Gly Leu Glu Gly Ala Ser
 50 55 60
 Glu Ser Pro Tyr Asp Arg Ala Val Leu Ile Ser Ala Cys Glu Arg Gly
 65 70 75 80
 Cys Arg Leu Phe Ser Ile Cys Arg Phe Val Ala Arg Ser Ser Lys Pro
 85 90 95
 Asn Ala Thr Gln Thr Glu Cys Glu Ala Ala Cys Val Glu Ala Tyr Val
 100 105 110
 Lys Glu Ala Glu Gln Gln Ala Cys Ser His Gly Cys Trp Ser Gln Pro
 115 120 125
 Ala Glu Pro Glu Pro Glu Gln Lys Arg Lys Val Leu Glu Ala Pro Ser
 130 135 140
 Gly Ala Leu Ser Leu Leu Asp Leu Phe Ser Thr Leu Cys Asn Asp Leu
 145 150 155 160
 Val Asn Ser Ala Gln Gly Phe Val Ser Ser Thr Trp Thr Tyr Tyr Leu
 165 170 175
 Gln Thr Asp Asn Gly Lys Val Val Val Phe Gln Thr Gln Pro Ile Val
 180 185 190
 Glu Ser Leu Gly Phe Gln Gly Gly Arg Leu Gln Arg Val Glu Val Thr
 195 200 205
 Trp Arg Gly Ser His Pro Glu Ala Leu Glu Val His Val Asp Pro Val
 210 215 220
 Gly Pro Leu Asp Lys Val Arg Lys Ala Lys Ile Arg Val Lys Thr Ser
 225 230 235 240
 Ser Lys Ala Lys Val Glu Ser Glu Glu Pro Gln Asp Asn Asp Phe Leu
 245 250 255
 Ser Cys Met Ser Arg Arg Ser Gly Leu Pro Arg Trp Ile Leu Ala Cys
 260 265 270
 Cys Leu Phe Leu Ser Val Leu Val Met Leu Trp Leu Ser Cys Ser Thr
 275 280 285
 Leu Val Thr Ala Pro Gly Gln His Leu Lys Phe Gln Pro Leu Thr Leu
 290 295 300
 Glu Gln His Lys Gly Phe Met Met Glu Pro Asp Trp Pro Leu Tyr Pro
 305 310 315 320

Pro Pro Ser His Ala Cys Glu Asp Ser Leu Pro Pro Tyr Lys Leu Lys
 325 330 335

Leu Asp Leu Thr Lys Leu
 340

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 671 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGGGCGGCG GAGTAGCAAG TGGCCATGGG GAGCCTCAGC GGTCTGCGCC TGGCAGCAGG	60
AAGCTGTTTT AGGTTATGTG AAAGAGATGT TTCCTCATCT CTAAGGCTTA CCAGAAGCTC	120
TGATTTGAAG AGAATAAATG GATTTTGCAC AAAACCACAG GAAAGTCCCG GAGCTCCATC	180
CCGCACTTAC AACAGAGTGC CTTTACACAA ACCTACGGAT TGGCAGAAAA AGATCCTCAT	240
ATGGTCAGGT CGCTTCAAAA AGGAAGATGA AATCCCAGAG ACTGTCTCGT TGGAGATGCT	300
TGATGCTGCA AAGAACAAGA TGCGAGTGAA GATCAGCTAT CTAATGATTG CCCTGACGGT	360
GGTAGGATGC ATCTTCATGG TTATTGAGGG CAAGAAGGCT GCCCAAAGAC ACGAGACTTT	420
AACAAGCTTG AACTTAGAAA AGAAAGCTCG TCTGAAAGAG GAAGCAGCTA TGAAGGCCAA	480
AACAGAGTAG CAGAGGTATC CGTGTTGGCT GGATTTTGAA AATCCAGGAA TTATGTTATA	540
ACGTGCCTGT ATTAAAAAGG ATGTGGTATG AGGATCCATT TCATAAAGTA TGATTTGCCC	600
AAACCTGTAC CATTTCCGTA TTTCTGCTGT AGAAGTAGAA ATAAATTTTC TTAAATAAAA	660
AAAAAAAAA A	671

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met	Gly	Ser	Leu	Ser	Gly	Leu	Arg	Leu	Ala	Ala	Gly	Ser	Cys	Phe	Arg	
1				5					10					15		
Leu	Cys	Glu	Arg	Asp	Val	Ser	Ser	Ser	Leu	Arg	Leu	Thr	Arg	Ser	Ser	
			20					25					30			
Asp	Leu	Lys	Arg	Ile	Asn	Gly	Phe	Cys	Thr	Lys	Pro	Gln	Glu	Ser	Pro	
		35					40					45				
Gly	Ala	Pro	Ser	Arg	Thr	Tyr	Asn	Arg	Val	Pro	Leu	His	Lys	Pro	Thr	
	50					55					60					
Asp	Trp	Gln	Lys	Lys	Ile	Leu	Ile	Trp	Ser	Gly	Arg	Phe	Lys	Lys	Glu	
65					70					75					80	
Asp	Glu	Ile	Pro	Glu	Thr	Val	Ser	Leu	Glu	Met	Leu	Asp	Ala	Ala	Lys	
				85					90					95		
Asn	Lys	Met	Arg	Val	Lys	Ile	Ser	Tyr	Leu	Met	Ile	Ala	Leu	Thr	Val	
			100					105					110			
Val	Gly	Cys	Ile	Phe	Met	Val	Ile	Glu	Gly	Lys	Lys	Ala	Ala	Gln	Arg	
		115					120					125				
His	Glu	Thr	Leu	Thr	Ser	Leu	Asn	Leu	Glu	Lys	Lys	Ala	Arg	Leu	Lys	
	130					135						140				
Glu	Glu	Ala	Ala	Met	Lys	Ala	Lys	Thr	Glu							
145					150											

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1056 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CACAAGAGGA GTTACTTGTT CCAGCCTCCT GTGTGGACTG CTTTCCTATC AAAGCACCTT	60
AGACATGCAC GAGGAAGAAA TATACACCTC TCTTCAGTGG GATAGCCCAG CACCAGACAC	120
TTACCAGAAA TGTCTGTCTT CCAACAAATG TTCAGGAGCA TGCTGTCTTG TGATGGTGAT	180
TTCATGTGTT TTCTGCATGG GATTATTAAC GGCATCCATT TTCTTGGGCG TCAAGTTGTT	240
GCAGGTGTCC ACCATTGCGA TGCAGCAGCA AGAAAACTC ATCCAACAAG AGAGGGCACT	300

GCTAAACTTT ACAGAATGGA AGAGAAGCTG TGCCCTTCAG ATGAAATATT GCCAAGCCTT 360
CATGCAAAAC TCATTAAGTT CAGGATTTTA TCACTGGCAG CTTGAGGAAG ATTAAGGAA 420
GCTATGATTA CTGGGTGGGG TTGTCTCAGG ATGGACACAG CGGACGCTGG CTTTGGCAAG 480
ATGGCTCCTC TCCTTCTCCT GGCTGTGTGC CAGCAGAGAG ATCCCAGTCA GCTAACCAAG 540
TCTGTGGATA CGTGAAAAGC AATTCCCTTC TTTCGTCTAA CTGCAGCACG TGGAAGTATT 600
TTATCTGTGA GAAGTATGCG TTGAGATCCT CTGTCTGAAA GAAATTGTGT TCAAAGTGTT 660
CTATTACACT GTTATTTGGA GCATGCCATT GGAAAACCCA CCCCCACCCC CCCTCAAAAA 720
AACAGAACAG TAAACCAAAA TGTGGGCCAT GAAATTAGCA ACCTGGGACT CAATAATACA 780
CTTGGAATA TTCTTCACA CCGTCCAGAT TTCATTTGAT GTTGTTTACA TTGCAAGAGT 840
AAAACCTTATT TAGAGCTACA GAAGACAAAA CCCTGAAGAG TTAAGAACAA ACGCAAGGAA 900
ATAATTTTAA TTGTTTAAAG CCCGGAATGA CTGTAACCTT CACACAAGGT ACGCATCTAT 960
GTTTTTGGGG GAGGTGATGT AGTTACAGCT GACTAATATT TTTAAAATAA ATAAATAAAT 1020
TTGGCCTTTA AAACCTCAAAA AAAAAAAAAA AAAAAA 1056

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	His	Glu	Glu	Glu	Ile	Tyr	Thr	Ser	Leu	Gln	Trp	Asp	Ser	Pro	Ala
1				5					10					15	
Pro	Asp	Thr	Tyr	Gln	Lys	Cys	Leu	Ser	Ser	Asn	Lys	Cys	Ser	Gly	Ala
			20					25					30		
Cys	Cys	Leu	Val	Met	Val	Ile	Ser	Cys	Val	Phe	Cys	Met	Gly	Leu	Leu
		35					40					45			
Thr	Ala	Ser	Ile	Phe	Leu	Gly	Val	Lys	Leu	Leu	Gln	Val	Ser	Thr	Ile
	50					55					60				
Ala	Met	Gln	Gln	Gln	Glu	Lys	Leu	Ile	Gln	Gln	Glu	Arg	Ala	Leu	Leu
65					70					75				80	
Asn	Phe	Thr	Glu	Trp	Lys	Arg	Ser	Cys	Ala	Leu	Gln	Met	Lys	Tyr	Cys
				85					90					95	

Gln Ala Phe Met Gln Asn Ser Leu Ser Ser Gly Phe Tyr His Trp Gln
 100 105 110

Leu Glu Glu Asp
 115

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

ANATTAGATC TGTTTCCATT TCCCAGGCA

29

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNGCGTGAGA TCAACTACTC TGCCTGTGA

29

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ANACAGGACC GAGTCGAGAA GCCAAAGAC

29

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ANGGGACAAT GCAAACGCAA GAGCTGGGC

29

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ANGAGGCATG TTTATCATCA GCCCTGCAG

29

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ANATTTGCCT TCTCAAAAGG GACACTGCT

29

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GNTGGGACTG GGAGGAGAGG AAGGATTTG

29

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GNAACGCCAT AAGCATGTCC TTCTAATGT

29

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CNTGAAATCA CCATCACAAG ACAGCATGC

29